

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 10, 2002, 15:34:02 ; Search time 23.93 Seconds
(Without alignments)
256.919 Million cell updates/sec

Title: US-09-555-534-2

Perfect score: 476
Sequence: 1 EPVDPRLERPMKHPGSGPQKTA.....VLSKQPTSGSGDPTGPKR 83

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

A.Geneseq_1101.*
1: /SIDSR/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /SIDSR/gcgdata/geneseq/geneseq/AA1981.DAT.*
3: /SIDSR/gcgdata/geneseq/geneseq/AA1982.DAT.*
4: /SIDSR/gcgdata/geneseq/geneseq/AA1983.DAT.*
5: /SIDSR/gcgdata/geneseq/geneseq/AA1984.DAT.*
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10: /SIDSR/gcgdata/geneseq/geneseq/AA1989.DAT.*
11: /SIDSR/gcgdata/geneseq/geneseq/AA1990.DAT.*
12: /SIDSR/gcgdata/geneseq/geneseq/AA1991.DAT.*
13: /SIDSR/gcgdata/geneseq/geneseq/AA1992.DAT.*
14: /SIDSR/gcgdata/geneseq/geneseq/AA1993.DAT.*
15: /SIDSR/gcgdata/geneseq/geneseq/AA1994.DAT.*
16: /SIDSR/gcgdata/geneseq/geneseq/AA1995.DAT.*
17: /SIDSR/gcgdata/geneseq/geneseq/AA1996.DAT.*
18: /SIDSR/gcgdata/geneseq/geneseq/AA1997.DAT.*
19: /SIDSR/gcgdata/geneseq/geneseq/AA1998.DAT.*
20: /SIDSR/gcgdata/geneseq/geneseq/AA1999.DAT.*
21: /SIDSR/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SIDSR/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	476	100.0	83	20	AAV22958	Wild type Tat amin
2	465	97.7	86	8	AAV70598	HIV virus recombin
3	465	97.7	86	10	AAV91903	Tat protein derive
4	465	97.7	86	10	AAV91905	CDNA for tat prote
5	465	97.7	86	10	AAV93140	Synthetic Tat prot
6	465	97.7	86	14	AAV38618	Sequence of the HI
7	465	97.7	86	17	AAV86625	HIV Tat. Human im
8	465	97.7	86	18	AAV31202	Human Immunodefici
9	465	97.7	86	18	AAV26443	HIV tat protein.
10	465	97.7	86	19	AAV71385	Amino acid sequenc
11	465	97.7	86	19	AAV76148	HIV Type I Tat pro

12	465	97.7	86	21	AAV96881	Human immunodefici
13	465	97.7	87	12	AAV13379	TAT protein. Synt
14	465	97.7	95	20	AAV02350	A representative H
15	465	97.7	95	22	AAV63232	Amino acid sequenc
16	465	97.7	302	20	AAV02351	A representative H
17	465	97.7	302	22	AAV63233	Amino acid sequenc
18	465	97.7	411	20	AAV02353	A representative L
19	465	97.7	411	22	AAV63235	Amino acid sequenc
20	465	97.7	413	20	AAV02355	A representative L
21	465	97.7	413	22	AAV63237	Amino acid sequenc
22	459	96.4	86	20	AAV22960	Lys41 mutant tat a
23	453	95.2	86	20	AAV22959	Cys22 mutant tat a
24	452	95.0	95	20	AAV02356	A representative H
25	452	95.0	95	22	AAV63238	Amino acid sequenc
26	452	95.0	302	20	AAV02357	A representative H
27	452	95.0	302	22	AAV63239	Amino acid sequenc
28	449	94.3	86	11	AAV02227	Sequence of the tr
29	449	94.3	86	16	AAV78742	Wild type Tat HIV
30	438	92.0	86	15	AAV48966	Diversified HIV-1
31	438	92.0	86	15	AAV57346	Peptide fragment o
32	436.5	91.7	83	20	AAV22961	RGD-delta mutant t
33	435	91.4	86	21	AAV10050	HIV-1 tat protein.
34	433	91.0	86	15	AAV48964	Full length Tat.
35	433	91.0	86	22	AAV64257	Human protein: Seq
36	430.5	90.4	83	20	AAV22962	Lys41-RGD-delta mu
37	429	90.1	86	22	AAV46679	HIV-1 Tat peptide
38	429	90.1	86	22	AAV46685	HIV-1 Tat peptide
39	420	88.2	86	16	AAV77542	Trans-dominant var
40	413	86.8	101	21	AAV14224	HIV Tat-SF162. Hu
41	401	84.2	102	21	AAV14225	HIV Tat-Cys22-SF16
42	397	83.4	101	12	AAV12259	HIV-1 strain OYI T
43	397	83.4	101	21	AAV30514	Sequence of the ta
44	394	82.8	86	22	AAV46681	HIV-1 Tat peptide
45	388	81.5	72	7	AAV60699	Trans-acting trans

ALIGNMENTS

RESULT 1
AAV22958 standard; Protein: 83 AA.
ID AAV22958:
AC AAV22958:
XX
XX 20-AUG-1999 (first entry)
DT
XX
XX Wild type Tat amino acid sequence of HIV-1.
DE
XX
XX HIV tat protein; AIDS: tumour; HIV infection; dendritic cell;
KW Kaposi's sarcoma cell; activated endothelial cell;
KW cytokine-activated endothelial cell; vaccine.
XX
XX Human immunodeficiency virus type 1.
OS
XX
XX W09927958-A2.
PN
XX
XX 10-JUN-1999.
PD
XX
XX 30-NOV-1998; 98WO-EP07721.
PF
XX
XX 01-DEC-1997; 97IT-RM00743.
PR
XX
XX (SUPE-) INST SUPERIORE DI SANITA.
PA
XX
XX Ensoli B;
PI
XX
XX WPI: 1999-385324/32.
DR N-PSDB; AAV81354.
DR
XX
XX Use of biologically active HIV Tat protein, fragments or mutants
PT
XX
XX Claim 8; Page 116; 150pp; English.
PS

XX The present sequence represents tat protein. The specification describes
CC the use of biologically active HIV Tat protein, fragments or mutants
CC for the prophylactic or therapeutic treatment of AIDS and tumours,
CC syndromes and symptoms associated with HIV infection. A biologically
CC active Tat protein, fragments and/or mutants and/or Tat DNA which is
CC capable of entering and localizing in the nuclei of activated endothelial
CC cells or dendritic cells and/or activating the proliferation, migration
CC and invasion of Kaposi's sarcoma (KS) cells and cytokine-activated
CC endothelial cells, is used as a vaccine. HIV-1 Tat or its mutants
CC in a biologically active form is able to induce a very strong immune
CC response against HIV, able to prevent infection or the development of
CC the disease and to permit efficient therapeutic strategies in
CC HIV-1-infected individuals.
XX
SQ Sequence 83 AA:

Query Match 100.0%; Score 476; DB 20; Length 83;
Best Local Similarity 100.0%; Pred. No. 8.8e-43;
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EPVDRLEPMKHPGSOPTACTNCTCKCCFHCQVCFITKAISYGRKKRRRPPGSG 60
Db 1 epvdprlepwmkhpqsgpkactnctckccfchqvcfilitkalsygrkkrrrrppgsg 60

OY 61 THQVSLSKOPTSOSRQDPTGPKE 83
Db 61 thqvsalskqptsqsgrdptgpke 83

RESULT 2
AAP70598
ID AAP70598 standard; protein; 86 AA.
XX
AC AAP70598;
XX
DT 17-MAR-1991 (first entry)
XX
DE HIV virus recombinant tat-3 protein.
XX
KW HIV virus; tat-3 protein; plasmid pAS1; plasmid pOTS-tatIIID;
KW plasmid pOTS-tatIII; AIDS; vaccine.
XX
OS Escherichia coli.
XX
PN MO8702989-A.
XX
PD 21-MAY-1987.
XX
PE 05-NOV-1986; 86WO-US02374.
XX
PF 06-NOV-1985; 85US-0795559.
XX
PR (SMIR) SMITHKLINE BECKMAN CORP.
PA (USDC) US DEPT COMMERCE.
XX
PI Aldovinnl A, Debouck CM, Rosenberg C, Wong-Staal F;
XX
DR WPI: 1987-150612/21.
DR N-PSDB: AAN70948.
XX
PT Recombinant TAT-3 gene of HTLV-III - for producing polypeptide(s)
PT for use in detection vaccination purification and therapy involving
PT HTLV-III infection.
XX
PS Claim 2; Page 14; 20pp; English.
XX
CC The sequence encodes the HIV virus tat-3 protein. The DNA
CC sequence encoding this protein is present in E. coli
CC plasmids pAS1, pOTS-tatIIID or pOTS-tatIII. Recombinant
CC tat-3 protein and its derivatives can be used in the
CC detection and therapy of HIV virus infection as well as an

CC an antigenic component of a vaccine.
XX
SQ Sequence 86 AA:

Query Match 97.7%; Score 465; DB 8; Length 86;
Best Local Similarity 97.6%; Pred. No. 1.3e-41;
Matches 83; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

OY 1 EPVDRLEPMKHPGSOPTACTNCTCKCCFHCQVCFITKA--ISYGRKKRRRPPGSG 58
Db 2 epvdprlepwmkhpqsgpkactnctckccfchqvcfilitkalsygrkkrrrrppg 61

OY 59 SOTHQVSLSKOPTSOSRQDPTGPKE 83
Db 62 sqthqvsalskqptsqsgrdptgpke 86

RESULT 3
AAP91903
ID AAP91903 standard; protein; 86 AA.
XX
AC AAP91903;
XX
DT 12-MAY-1990 (first entry)
XX
DE Tat protein derived from human immuno-deficiency virus
DE (HIV: HTLV-III/LAV) cDNA.
XX
KW Recombinant vaccinia virus; HIV tat protein cDNA; HTLV-III;
KW LAV; AIDS; ARC.
XX
XX Human immunodeficiency virus.
XX
OS JPO1085072-A.
XX
PN 30-MAR-1989.
XX
PD 25-SEP-1987; 87JP-0240514.
XX
PE 25-SEP-1987; 87JP-0240514.
XX
PF 25-SEP-1987; 87JP-0240514.
XX
PR (KOKU-) KOKURITSU YOBO EISE (JAPG).
PA
XX
DR WPI: 1989-140769/19.
DR N-PSDB: AAN92430.
XX
PT Recombinant vaccinia virus
PT - has protein coding complementary DNA from human
PT immuno: deficiency virus in genome DNA domain
XX
PS Fig 4; page 420; 8pp; Japanese.
XX
CC All or part of it can be produced by recombinant vaccinia virus by
CC integrating it into the genome region nonessential for vaccinia virus
CC proliferation and then infecting animal cells with the recombinant virus.
CC Tat protein can be used to diagnose HIV infection and for prophylaxis
CC for AIDS or ARC patients. It can also be used to develop a live vaccine
CC using temperature-sensitive Lister strain of vaccinia virus.
XX
SQ Sequence 86 AA:

Query Match 97.7%; Score 465; DB 10; Length 86;
Best Local Similarity 97.6%; Pred. No. 1.3e-41;
Matches 83; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

OY 1 EPVDRLEPMKHPGSOPTACTNCTCKCCFHCQVCFITKA--ISYGRKKRRRPPGSG 58
Db 2 epvdprlepwmkhpqsgpkactnctckccfchqvcfilitkalsygrkkrrrrppg 61

OY 59 SOTHQVSLSKOPTSOSRQDPTGPKE 83
Db 62 sqthqvsalskqptsqsgrdptgpke 86

Db	62	sqtghvslskptsgsrjgdpitgpke	86
<hr/>			
RESULT	4		
ID	AAP91905	AAP91905 standard; protein: 86 AA.	
XX	AAP91905;		
AC			
XX			
DT	12-MAY-1990	(first entry)	
XX			
DE	cDNA for tat protein of human immunodeficiency virus (HIV).		
XX			
KW	tat protein; HIV; recombinant vaccinia virus.		
OS	Human immunodeficiency virus.		
XX			
FH	Key	Location/Qualifiers	
FT	CDS	46..306	
FT		/*tag= a	
XX			
PN	JP01085092-A.		
XX			
PD	30-MAR-1989.		
XX			
PE	25-SEP-1987;	87JP-0240513.	
XX			
PR	25-SEP-1987;	87JP-0240513.	
XX			
PA	(KOKU-) KOKURITSU YOBO EISEI (JAPG).		
XX			
DR	WPI: 1989-140777/19.		
N-PSDB:	AAP91905.		
XX			
PT	prodn. of protein(s)		
PT	- using recombinant vaccinia viruses contg. protein of		
PT	Human Immunodeficiency Virus		
XX			
PS	Fig 5; page 863; 9pp; Japanese.		
XX			
CC	It is inserted into the genome of vaccinia viruses in a		
CC	region which is not essential for their propagation to create recombinant		
CC	vaccinia viruses. These viruses are propagated in animal cells together		
CC	with recombinant vaccinia viruses which contain DNA coding for a useful		
CC	protein, for example, human growth hormone, insulin, interferons,		
CC	interleukin-2; haemagglutination factor, hepatitis-B surface antigen,		
CC	amylase, protease. The presence of tat protein assists the mass-		
CC	production of the useful protein.		
SQ	Sequence	86 AA:	
<hr/>			
Query Match	97.7%;	Score 465;	DB 10; Length 86;
Best Local Similarity	97.6%;	Pred. No. 1.3e-41;	
Matches	83; Conservative	0; Mismatches	0; Indels 2; Gaps 1.
OY	1	EPVDRLPPMKHPGSOPHTACTNCKCKKCCEFCGYCETITKA--ISVGRKKRRORRRPPQG	58
Db	2	EPVDRLPPMKHPKSQPKTACCNCYCCKKCCFICIKALGISYGRKKRTRTPPG	61
OY	59	SQTGHVSLSKOPTSSRSRGDPNGPKE	83
Db	62	SQTGHVSLSKPTSGSRJGDPITGPKE	86
<hr/>			
RESULT	5		
ID	AAP93140	AAP93140 standard; protein: 86 AA.	
XX	AAP93140;		
AC			
XX			
DT	21-MAR-1990	(first entry)	
XX			

DE	Synthetic TAT protein.
KW	TAT protein; HIV-1; tat gene; trans-activator; anti-terminator;
XX	
PN	MO8909824-A.
XX	
PD	19-OCT-1989.
XX	
PF	14-APR-1989; 89MO-GH00384.
XX	
PR	15-APR-1988; 88GB-0008892.
XX	
PA	(BRB1-) BRITISH BIO TECHNOLOGY.
XX	
P1	Edwards RM, Adams SE;
XX	
DR	WPI: 1989-324229/44.
DR	N-PSDB; AAN91837.
XX	
PT	Synthesis of double stranded DNA, esp. TAT gene of HIV - by prepreg. DNA
XX	contg. a single and double stranded portion and in vivo gap repair.
FS	Disclosure; fig.2; 23pp; English.
CC	The synthetic tat DNA encoding this protein has useful restriction sites
CC	to facilitate modification for structural and immunological studies. TAT
CC	is a transactivator involved in the activation of HIV long terminal
CC	repeat, acting as an anti-terminator.
XX	
QO	Sequence 86 AA;

	Query Match	97.7%;	Score 465;	DB 10;	Length 86;
	Best Local Similarity	97.6%;	Pred.No. 1.3e-41;		
	Matches 83;	Conservative	0;	Mismatches 0;	Indels 2; Gaps
OY	1 EPVPRLEPMKHHGSPQPTACTNCYCCKCCFHCQVCFLTKA--TSYGRKKRRORRRPPQG	51			
Db	2 epvdpriepkhhpgsqpkactncycckccfchcfcyqcfiltkaiglsygkrkkrrgrrppg	6			
OY	59 SQRHQSLSKOPTSQSRGDETPGRE	83			
Db	62 sqthqvslskpqtsgrgdtpgke	86			
RESULT	6				
AAR38618					
ID	AAR38618 standard; protein; 86 AA.				
AC					
XX	AAR38618;				
DT	13-DEC-1993 (first entry)				
XX					
DE	Sequence of the HIV-1 TAR protein.				
KW	Human immunodeficiency virus 1; HIV-1; TAR protein; transactivator;				
KM	long terminal repeat; transactivation response element; TAR;				
XX	RNA binding; RNA cleavage.				
OS	Human immunodeficiency virus 1.				
XX					
Key	Location/Qualifiers				
FT	Domain	49..57			
FT	/label= nuclear targeting domain				
FT	Region	49..72			
FT	/note= "proteolytic product of wt TAR protein				
FT	which binds specifically to TAR-element-				
FT	config. RNA"				
XX					
EN	MO9312234-A.				
XX					
PD	24-JUN-1993.				
XX					

PF 11-DEC-1992; 92WO-US10770.
 XX
 PR 13-DEC-1991; 91US-0808452.
 PR 21-JAN-1992; 92US-0826934.
 XX
 PA (SRI) SRI INT.
 XX
 PI Jayasena SD, Johnston BH;
 XX
 DR WPI: 1993-214176/26.
 XX
 XX Viral polypeptide(s) with site-specific RNA binding - contain
 PT motley to cleave RNA backbone and are used to inhibit HIV antigen
 PT expression in infected cells
 XX
 PS Claim 2; Figure 2A; 94pp; English.
 XX
 CC TAR is a potent transactivator of long terminal repeat (LTR)-
 CC directed viral gene expression. TAR-induced transactivation requires
 CC the present of the TAR (transactivation response) element, located
 CC at the 5'UTR of the viral RNA element. The sequence of RNA target
 CC molecules were chosen based on previous studies characterising the
 CC binding properties of the HIV-encoded TAR protein and the TAR target
 CC region from both HIV-1 and HIV-2. HIV-1 TAR is the 57-nt RNA stem-
 CC loop structure found in HIV-1 mRNA (nt 1-57). The RNA substrate is
 CC given in AAQ44139.
 CC
 SQ Sequence 86 AA;

Query Match 97.7%; Score 465; DB 14; Length 86;
 Best Local Similarity 97.6%; Pred. No. 1.3e-41;
 Matches 83; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 EPVDPRLPMKHPGSPQPTACTNCYCKKCFHCQVCFITKA--ISYGRKKRRRRRRPQG 58
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 2 epvdpriepwkhpgsqpktaactncycckcfcfhqvcfllkalgsygrkkrrrrppg 61
 QY 59 SQTHOVSLSKOPTSQSRGDPGPK 83
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 62 sqthqvslskqptsqsrqdpdpkpe 86

RESULT 7
 AAR86625
 ID AAR86625 standard; Protein; 86 AA.
 XX
 AC AAR86625;
 XX
 DT 28-JUN-1996 (first entry)
 XX
 DE HIV TAT.
 XX
 KW Immunogen; cellular uptake region; transactivating protein; TAR; HIV;
 KW viraemia; antibody.
 XX
 OS Human immunodeficiency virus.
 XX
 FH Key Location/Qualifiers
 FT Peptide 46..63
 FT /note= "Cellular uptake region"
 XX
 PN WO953199-A1.
 XX
 PD 30-NOV-1995.
 XX
 PE 16-MAY-1995; 95WO-US06077.
 XX
 PR 23-MAY-1994; 94US-0247991.
 XX
 PR (IMMU-) IMMUNOGIOLOGY RES INST INC.
 PA
 PI Culler MD, Goldstein G, Shenbagamurthi P;

XX
 DR WPI: 1996-049298/05.
 DR N-PSDB: AAT06634.
 XX
 PT Immunogen containing cellular uptake region of viral TAR protein -
 PT induces high antibody titre against TAR, partic. for preventing or
 PT treating HIV infection
 XX
 PS Disclosure; Figure 1; 54pp; English.
 XX
 CC This sequence represents the HIV transactivating protein, TAR. The
 CC sequences given in AAR86601-19 are immunogens derived from the cellular
 CC uptake region of this protein. These peptides are based on the region
 CC comprising amino acids 46-63. The immunogenic peptides are used to
 CC protect against infection by HIV. They may also be used to reduce
 CC viraemia in already infected patients. These immunogens may be used
 CC to identify, or generate, antibodies specific for TAR.
 CC
 SQ Sequence 86 AA;

Query Match 97.7%; Score 465; DB 17; Length 86;
 Best Local Similarity 97.6%; Pred. No. 1.3e-41;
 Matches 83; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 EPVDPRLPMKHPGSPQPTACTNCYCKKCFHCQVCFITKA--ISYGRKKRRRRRRPQG 58
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 2 epvdpriepwkhpgsqpktaactncycckcfcfhqvcfllkalgsygrkkrrrrppg 61
 QY 59 SQTHOVSLSKOPTSQSRGDPGPK 83
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 62 sqthqvslskqptsqsrqdpdpkpe 86

RESULT 8
 AAW31202
 ID AAW31202 standard; protein; 86 AA.
 XX
 AC AAW31202;
 XX
 DT 20-MAR-1998 (first entry)
 XX
 DE Human Immunodeficiency Virus Type 1 Tat protein.
 XX
 KW Human immunodeficiency virus; HIV Type 1; Tat protein;
 KW cargo molecules; intracellular delivery; fusion protein;
 KW therapeutic; prophylactic; diagnostic; transport polypeptide.
 XX
 OS Human immunodeficiency virus type 1.
 XX
 FH Key Location/Qualifiers
 FT Region 22..36
 FT /label= cysteine-rich
 FT Region 49..57
 FT /label= basic_region
 FT Domain 73..86
 FT /label= carboxy_terminal_domain
 XX
 PN US5674980-A.
 XX
 PD 07-OCT-1997.
 XX
 PF 21-DEC-1989; 89US-0454450.
 XX
 PR 28-APR-1994; 94US-0235403.
 PR 21-DEC-1989; 89US-0454450.
 PR 02-JAN-1991; 91US-0636662.
 PR 21-AUG-1992; 92US-0934375.
 PR 19-AUG-1993; 93WO-US07833.
 PR 24-NOV-1993; 93US-0158015.
 PR 25-MAY-1995; 95US-0450098.
 XX
 PA (BARS/) BARSOM J G.

PD 03-SEP-1998.
 XX
 PF 25-FEB-1998; 98WO-US03689.
 XX
 PR 26-FEB-1997; 97US-0807014.
 XX
 PA (CIBL-) CIBLEX CORP.
 XX
 PI Baird A, Florikiewicz RZ;
 XX
 DR WPI: 1998-495377/42.
 DR N-PSDB; AAV60345.
 XX
 PF Inhibiting export of leaderless protein with agent that inhibits
 PF binding to transporter protein - especially for treating
 PF angiogenesis and restenosis by preventing export of fibroblast
 PF growth factor; also methods for identifying leaderless proteins and
 PF their transporters
 XX
 PS Claim 2; Page 70; 116pp; English.
 XX
 CC The present sequence represents Human immunodeficiency virus (HIV) Tat
 CC 85, a leaderless protein. A leaderless protein refers to a protein that
 CC is found in an extracellular environment, but lacks a canonical leader
 CC sequence. The specification describes a method for inhibiting export of
 CC a leaderless protein from a cell. The method comprises treating
 CC the cell with an agent that inhibits binding between the leaderless
 CC protein and a transport molecule. Treatment with the inhibiting agent
 CC is specifically used to treat angiogenesis and restenosis, i.e. where
 CC expression of FGF-2 is inhibited, and the agent is applied to endothelial
 CC or smooth muscle cells. Other applications are treatment of tumors
 CC (melanoma, teratocarcinoma, ovarian carcinoma, bladder cancer and
 CC neuroblastoma), inflammation, cell proliferation, complications of
 CC diabetes (e.g. retinopathy), viral, bacterial or fungal infections,
 CC polycystic kidney disease and atherosclerosis.
 XX
 SQ Sequence 86 AA;

Query Match 97.7%; Score 465; DB 19; Length 86;
 Best Local Similarity 97.6%; Pred. No. 1.3e-41;

Matches 83; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

OY 1 EPVDRLEPWRKHPGSOPTACTNCYCKKCCFHQCVCFTTKA--ISYGRKKRRRRRPPG 58
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 2 epvdrlepwkhpqsgpqtactncycckkccfhqcvcfttkalgsygrkkrrrrppg 61
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

OY 59 SQTHGVSLSKOPTSOSRSDPTGPK 83
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 62 sqthgvslskqptsqsdgdpkpke 86
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

RESULT 11

AAW76148
 ID AAW76148 standard; protein; 86 AA.

AC AAW76148;

DT 24-NOV-1998 (first entry)

DE HIV Type I Tat protein.

KW Tat protein; cargo molecule; therapy; diagnosis; transport protein;
 fusion protein; human papillomavirus E2 repressor; target cell.

OS Human immunodeficiency virus type 1.

PN US5804604-A.

PD 08-SEP-1998.

PF 25-MAY-1995; 95US-0450236.

XX

PR 28-APR-1994; 94US-0235403.
 PR 21-DEC-1989; 89US-0454450.
 PR 02-JAN-1991; 91US-0636662.
 PR 19-AUG-1993; 93WO-US07833.
 PR 24-NOV-1993; 93US-0156015.
 PR 25-MAY-1995; 95US-0450236.
 XX
 PA (BIOJ) BIOGEN INC.
 XX
 PI Barsom JG, Fawell SE, Frankel A, Pabo C, Pepinsky RB;
 XX
 DR WPI: 1998-505702/43.
 XX
 PF HIV tat-derived transport fusion proteins - used to deliver
 PF biological active molecules e.g. peptides) or nucleic acids,
 PF specifically into cytoplasm or nuclei of cells
 XX
 PS Disclosure; Fig 1; 83pp; English.

This sequence represents the human immunodeficiency virus (HIV) Type I
 Tat protein which is used in a method for the delivery of biologically
 active cargo molecules into the cytoplasm and nuclei of cells, for
 therapeutic, prophylactic or diagnostic purposes. This is accomplished
 by the presence of a small, basic section of tat transport protein of
 HIV. This is used as it is this protein which is observed to cause human
 cells in culture to take up HIV. The method involves the use of a cargo
 moiety in combination with a transport moiety usually in the form of a
 fusion protein. The cargo moiety is a human papillomavirus E2 repressor
 that retains its biological activity after delivery into a target cell
 and where the transport moiety is one of following HIV tat protein
 fragments (a) aa 47-58, (b) aa 47-72, (c) 38-72, (d) aa 38-58, (e)
 aa 37-58, (f) aa 1-21 and 38-72, (g) aa 47-62 or aa 38-62. The proteins
 allow delivery of specific peptides into cells at high concentrations
 due to use of existing transporters. Previous methods of delivery
 include bombardment and transforming, which only allow a fraction of the
 cell population to be infected and can additionally damage cells as
 they cause physical opening of the cell walls/membranes to allow entry.

Sequence 86 AA;

Query Match 97.7%; Score 465; DB 19; Length 86;
 Best Local Similarity 97.6%; Pred. No. 1.3e-41;

Matches 83; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

OY 1 EPVDRLEPWRKHPGSOPTACTNCYCKKCCFHQCVCFTTKA--ISYGRKKRRRRRPPG 58
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 2 epvdrlepwkhpqsgpqtactncycckkccfhqcvcfttkalgsygrkkrrrrppg 61
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

OY 59 SQTHGVSLSKOPTSOSRSDPTGPK 83
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 62 sqthgvslskqptsqsdgdpkpke 86
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

RESULT 12

AAAY6881
 ID AAY6881 standard; Protein; 86 AA.

AC AAY6881;

DT 31-OCT-2000 (first entry)

DE Human immunodeficiency virus Tat 85.

KW Human immunodeficiency virus; HIV; Tat 85; transport molecule; goigi;
 leaderless; endoplasmic reticulum; protein export; detection; inhibitor.

OS Human immunodeficiency virus type 1.

PN Key Location/Qualifiers

PF Misc-difference 53

FT Misc-difference 80

FT

FT /note= "Encoded by GAA"
 XX
 PN US6083706-A.
 XX
 PD 04-JUL-2000.
 XX
 PF 25-FEB-1998; 98US-0030613.
 XX
 PR 26-FEB-1997; 97US-0807014.
 XX
 PA (CIBL-) CIBLEX CORP.
 XX
 PI Baird A, Florkiewicz RZ;
 XX
 DR WPI: 2000-464338/40.
 DR N-PSDB; AAA53572.
 XX
 PT Detecting transport molecules, useful for identifying proteins that
 PT mediate leaderless protein export across cell membranes, by contacting
 PT cell extracts with a fusion protein of leaderless protein and a tag to
 PT form a complex
 XX
 PS Disclosure; Column 55-56; 64pp; English.
 XX
 CC Detecting a transport molecule involved in non-endoplasmic reticulum
 CC (ER)/Golgi leaderless protein export, comprises contacting test cell
 CC extracts or membranes with a fusion protein of a leaderless protein and
 CC a tag to form a complex of the fusion protein bound to the transport
 CC molecule, and detecting the transport molecule in an isolated complex.
 CC The leaderless protein is a protein found in the extracellular
 CC environment that lacks a canonical leader sequence, interleukin (IL)
 CC 1-alpha, or 1-beta, fibroblast growth factor (FGF) 1 or 2, human
 CC immunodeficiency virus (HIV) tat, platelet-derived endothelial cell
 CC growth factor (PD-ECGF), ciliary neurotrophic factor (CNTF), sciatic
 CC nerve growth-promoting activity, vas deferens protein, transglutaminase,
 CC L-14 lectin, factor XIIIa, thiodoxin-like protein (ADP), thyrosin,
 CC parathymosin, mammary-derived growth inhibitor, galectin or rhodanase.
 CC The method is used to detect proteins, complexes of proteins, or parts of
 CC a larger complex, that bind to and mediate the transport of leaderless
 CC proteins, e.g. Na⁺/K⁺ ATPase which is an integral membrane protein
 CC responsible for transporting sodium and potassium ions across the cell
 CC membrane using ATP as the driving force. Transport molecules detected by
 CC the method are used in assays to identify inhibitors of the interaction
 CC with a leaderless protein.
 CC
 XX
 SQ Sequence 86 AA;
 XX
 Query Match 97.7%; Score 465; DB 21; Length 86;
 Best Local Similarity 97.6%; Pred. No. 1.3e-41;
 Matches 83; Conservative 0; Mismatches 0; Indels 2; Gaps 1;
 OY 1 EPVDPRLPEPKHPSQPTACTNCTCYCKKCFHCQVCFITKA--ISYRKRRRORRRPQG 58
 DB 2 epvdpriepkhp9sqptactncycckcfcqvcfcltkalgisygrkrrgrrppqg 61
 OY 59 SQTHQVSLSKOPTSQSRGDPGPK 83
 DB 62 sqthqvslskqpsqsrgrdptgpke 86
 XX
 RESULT 13
 AAR13379
 ID AAR13379 standard; Protein; 87 AA.
 XX
 AC AAR13379;
 XX
 DT 23-OCT-1991 (first entry)
 XX
 DE TAT protein.
 XX
 KM HIV; AIDS.
 XX

OS Synthetic.
 XX
 PN EP441582-A.
 XX
 PD 14-AUG-1991.
 XX
 PF 04-FEB-1991; 91EP-0300903.
 XX
 PR 09-FEB-1990; 90GB-0003010.
 XX
 PA (GLAX) GLAXO GROUP LTD.
 XX
 PI Dykes CW, Ernst JF, Hobden AN;
 XX
 DR WPI: 1991-240122/33.
 DR N-PSDB; AAQ13188.
 XX
 PT Gene expression system for yeast cells - with TAT protein
 PT mediated expression under the control of a HIV regulatory control
 PT sequence.
 XX
 PS Disclosure; Page 10; 26pp; English.
 XX
 CC The TAT protein here is encoded by the synthetic tat gene but is
 CC identical to the TAT protein found in HIV. The expression of the TAT
 CC protein in transformed yeast enables TAT inhibitory agents to be
 CC screened to obtain potential anti-viral agents esp. anti-HIV
 CC therapeutic agents.
 XX
 SQ Sequence 87 AA;
 XX
 Query Match 97.7%; Score 465; DB 12; Length 87;
 Best Local Similarity 97.6%; Pred. No. 1.3e-41;
 Matches 83; Conservative 0; Mismatches 0; Indels 2; Gaps 1;
 OY 1 EPVDPRLPEPKHPSQPTACTNCTCYCKKCFHCQVCFITKA--ISYRKRRRORRRPQG 58
 DB 2 epvdpriepkhp9sqptactncycckcfcqvcfcltkalgisygrkrrgrrppqg 61
 OY 59 SQTHQVSLSKOPTSQSRGDPGPK 83
 DB 62 sqthqvslskqpsqsrgrdptgpke 86
 XX
 RESULT 14
 AAY02350
 ID AAY02350 standard; Protein; 95 AA.
 XX
 AC AAY02350;
 XX
 DT 09-JUL-1999 (first entry)
 XX
 DE A representative HIV-1 Tat-His protein.
 XX
 KM HIV nef gene; fusion protein; HIV nef gene; Nef protein; Tat protein;
 KM vaccine; HIV infection; protein D.
 XX
 OS Synthetic.
 OS human immunodeficiency virus type 1.
 XX
 PN WO916884-A1.
 XX
 PD 08-APR-1999.
 XX
 PF 17-SEP-1998; 98WO-EP06040.
 XX
 PR 26-SEP-1997; 97GB-0020585.
 XX
 PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
 XX
 PI Bruck C, Godart SAG, Marchand M;
 XX

DR WPI: 1999-302282/25.
 DR N-PSDB: AAX33686.
 XX
 PT HIV Tat or Nef protein linked to a fusion partner
 XX
 PS Disclosure: Fig 2: 66pp: English.
 XX
 CC The present sequence represents a representative HIV-1 Tat-His protein.
 CC The protein is used in the creation of the fusion proteins of
 CC the invention, in conjunction with a fusion partner (e.g. protein D).
 CC The specification also describes fusion proteins comprising HIV-1 Nef
 CC protein. The fusion protein can be used in a vaccine to prevent HIV
 CC infection.
 XX
 SQ Sequence 95 AA:
 XX
 Query Match 97.7%; Score 465; DB 20; Length 95;
 Best Local Similarity 97.6%; Pred. No. 1.4e-41;
 Matches 83; Conservative 0; Mismatches 0; Indels 2; Gaps 1;
 QY 1 EPVDPRLPEPMKHPGSOPTACTNCCYCKKCFHCQVCFITKA--ISYGRKKRRRRRRPPQG 58
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 Db 2 EPVDPRLPEPMKHPGSOPTACTNCCYCKKCFHCQVCFITKAISYGRKKRRRRRRPPQG 61
 QY 59 SOTHQVSLSKOPTSQSRGDPGTGPK 83
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 62 sqthqvsiskpptsqsrqdtgpk 86
 RESULT 15
 AAG63232
 ID AAG63232 standard: protein; 95 AA.
 XX
 AC AAG63232;
 XX
 DT 01-OCT-2001 (first entry)
 XX
 DE Amino acid sequence of a His-tagged Tat protein of HIV.
 XX
 KW HIV; nef gene; tat gene; vaccine; gp120 gene; HIV viral load.
 XX
 OS Synthetic.
 OS Human immunodeficiency virus.
 OS
 PN WO200154719-A2.
 XX
 PD 02-AUG-2001.
 XX
 PF 29-JAN-2001; 2001WO-EP00944.
 XX
 PR 31-JAN-2000; 2000GB-0002200.
 PR 14-APR-2000; 2000GB-0009336.
 PR 06-JUN-2000; 2000GB-0013806.
 PR 28-JUN-2000; 2000WO-EP05998.
 XX
 PA (SMK) SMITHKLINE BEECHAM BIOLOGICALS.
 XX
 PI Voss G;
 XX
 DR WPI: 2001-476172/51.
 DR N-PSDB: AAH42876.
 XX
 PT New use of a human immunodeficiency virus (HIV) Tat, or Nef, or Nef
 PT linked to Tat (Nef-Tat) protein or polynucleotide and an HIV gp120
 PT protein or polynucleotide for the manufacture of a vaccine -
 XX
 PS Disclosure: Fig 1: 90pp: English.
 XX
 CC The present sequence represents a His-tagged Tat protein of HIV. The
 CC protein is expressed in the yeast *Pichia pastoris*, and is used to
 CC produce the vaccine in the invention. The specification describes
 CC the use of HIV Tat, HIV Nef, or Nef-Tat; and HIV gp120 in the

CC manufacture of a vaccine. The vaccine is used for the prophylactic or
 CC therapeutic immunization of humans against HIV. Tat, Nef or Nef-Tat act
 CC in synergy with gp120 in the treatment and prevention of HIV. The
 CC vaccine reduces the HIV viral load in HIV infected humans and results
 CC in a maintenance of CD4+ levels over those levels found in the absence
 CC of vaccination with HIV Tat, Nef or Nef-Tat and HIV gp120.
 XX
 SQ Sequence 95 AA:

Query Match 97.7%; Score 465; DB 22; Length 95;
 Best Local Similarity 97.6%; Pred. No. 1.4e-41;
 Matches 83; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 EPVDPRLPEPMKHPGSOPTACTNCCYCKKCFHCQVCFITKA--ISYGRKKRRRRRRPPQG 58
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 2 EPVDPRLPEPMKHPGSOPTACTNCCYCKKCFHCQVCFITKAISYGRKKRRRRRRPPQG 61
 QY 59 SOTHQVSLSKOPTSQSRGDPGTGPK 83
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 Db 62 sqthqvsiskpptsqsrqdtgpk 86

Search completed: January 10, 2002, 15:34:34
 Job time: 32 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 10, 2002, 15:34:02 ; Search time 12.59 Seconds

(without alignments)
148.354 Million cell updates/sec

Title: US-09-555-534-2

Perfect score: 476
Sequence: 1 EVDPRLEPMKHNPSQPKTA.....VSLSKPTSGSRGDPRTGPK 83

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

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4: /cgn2_6/prodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/prodata/2/1aa/PCTUS.COMB.pep:*
6: /cgn2_6/prodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	465	97.7	86	1	US-08-450-257-1
2	465	97.7	86	1	US-08-450-246-1
3	465	97.7	86	1	US-08-450-098-1
4	465	97.7	86	1	US-08-451-233-1
5	465	97.7	86	1	US-08-450-236-1
6	465	97.7	86	3	US-07-808-452-1
7	465	97.7	86	3	US-09-030-613-1
8	465	97.7	86	4	US-09-124-800-6
9	465	97.7	86	4	US-09-451-905-19
10	465	97.7	86	5	PCT-US92-10770-1
11	465	97.7	86	5	PCT-US95-06077-2
12	449	94.3	86	2	US-08-505-210-1
13	449	94.3	86	4	US-09-099-333-1
14	434	91.2	82	1	US-08-053-079A-15
15	388	81.5	72	3	US-09-030-613-17
16	388	81.5	72	4	US-09-451-905-17
17	364	76.5	72	4	US-08-893-853-1
18	364	76.5	72	4	US-09-113-921-1
19	339	71.2	312	1	US-08-094-128A-27
20	339	71.2	312	1	US-08-455-674-27
21	339	71.2	312	1	US-08-455-892-27
22	339	71.2	312	1	US-08-455-972-27
23	339	71.2	312	5	PCT-US92-00652-27
24	331	69.5	72	1	US-07-910-867B-2
25	310	65.1	72	1	US-07-910-867B-5
26	304	63.9	72	1	US-07-910-867B-3
27	290	60.9	72	1	US-07-910-867B-1

28	256	53.8	56	1	US-08-450-257-7	Sequence 7, App11
29	256	53.8	56	1	US-08-450-246-7	Sequence 7, App11
30	256	53.8	56	1	US-08-450-098-7	Sequence 7, App11
31	256	53.8	56	1	US-08-451-233-7	Sequence 7, App11
32	256	53.8	56	1	US-08-450-236-7	Sequence 7, App11
33	195	41.0	37	1	US-07-724-500B-22	Sequence 22, App1
34	176	37.0	106	6	5204258-4	Patent No. 5204258
35	166.5	35.0	157	1	US-08-450-257-60	Sequence 60, App1
36	166.5	35.0	157	1	US-08-450-246-60	Sequence 60, App1
37	166.5	35.0	157	1	US-08-450-098-60	Sequence 60, App1
38	166.5	35.0	157	1	US-08-451-233-60	Sequence 60, App1
39	166.5	35.0	157	1	US-08-450-236-60	Sequence 60, App1
40	166	34.9	36	1	US-08-450-257-2	Sequence 2, App11
41	166	34.9	36	1	US-08-450-246-2	Sequence 2, App11
42	166	34.9	36	1	US-08-450-098-2	Sequence 2, App11
43	166	34.9	36	1	US-08-451-233-2	Sequence 2, App11
44	166	34.9	36	1	US-08-450-236-2	Sequence 2, App11
45	159	33.4	36	5	PCT-US95-06077-15	Sequence 15, App1

ALIGNMENTS

RESULT 1
US-08-450-257-1
; Sequence 1, Application US/08450257
; Patent No. 5652122
; GENERAL INFORMATION:
; APPLICANT: FRANKEL, Alan
; APPLICANT: PABO, Carl
; APPLICANT: BARSODI, James G.
; APPLICANT: FAMELL, Stephen E.
; APPLICANT: PEPINSKY, R. B.
; TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,257
; FILING DATE: 25-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/235,403
; FILING DATE: 28-APR-1994
; APPLICATION NUMBER: US 07/934,375
; FILING DATE: 21-AUG-1992
; APPLICATION NUMBER: US 07/098,766
; FILING DATE: 28-JUL-1993
; APPLICATION NUMBER: PCT/US93/07833
; FILING DATE: 19-AUG-1993
; APPLICATION NUMBER: US 07/454,450
; FILING DATE: 21-DEC-1989
; APPLICATION NUMBER: US 07/636,662
; FILING DATE: 02-JAN-1991
; APPLICATION NUMBER: US 08/158,015
; FILING DATE: 24-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Haley Jr., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: B170 CIP 2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090

TELEX: 14-8367
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 86 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: human immunodeficiency virus
STRAIN: type 1
US-08-450-257-1

Query Match 97.7%; Score 465; DB 1; Length 86;
Best Local Similarity 97.6%; Pred. No. 6.4e-45;
Matches 83; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 EPVDPRLPEPMKHGSPKPTACTNCTCKKCFHCQVCFITKA--ISYGRKKRRRRRPPQG 58
|||||
DB 2 EPVDPRLPEPMKHGSPKPTACTNCTCKKCFHCQVCFITKALGISYGRKKRRRRRPPQG 61
|||||
QY 59 SOTHQVSLSKOPTSQSRGDPPTGPK 83
|||||
DB 62 SOTHQVSLSKOPTSQSRGDPPTGPK 86

RESULT 2
US-08-450-246-1
Sequence 1, Application US/08450246
Patent No. 5670617
GENERAL INFORMATION:
APPLICANT: FRANKEL, Alan
APPLICANT: PABO, Carl
APPLICANT: BARSOUM, James G.
APPLICANT: FAMELL, Stephen E.
APPLICANT: PEPIISKY, R. B.
TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,246
FILING DATE: 25-MAY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/235,403
FILING DATE: 28-APR-1994
APPLICATION NUMBER: US 07/934,375
FILING DATE: 21-AUG-1992
APPLICATION NUMBER: US 07/098,766
FILING DATE: 28-JUL-1993
APPLICATION NUMBER: PCT/US93/07833
FILING DATE: 19-AUG-1993
APPLICATION NUMBER: US 07/454,450
FILING DATE: 21-DEC-1989
APPLICATION NUMBER: US 07/636,662
FILING DATE: 02-JAN-1991
APPLICATION NUMBER: US 08/158,015
FILING DATE: 24-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B170 CIP 2

TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
TELEX: 14-8367
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 86 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: human immunodeficiency virus
STRAIN: type 1
US-08-450-246-1

Query Match 97.7%; Score 465; DB 1; Length 86;
Best Local Similarity 97.6%; Pred. No. 6.4e-45;
Matches 83; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 EPVDPRLPEPMKHGSPKPTACTNCTCKKCFHCQVCFITKA--ISYGRKKRRRRRPPQG 58
|||||
DB 2 EPVDPRLPEPMKHGSPKPTACTNCTCKKCFHCQVCFITKALGISYGRKKRRRRRPPQG 61
|||||
QY 59 SOTHQVSLSKOPTSQSRGDPPTGPK 83
|||||
DB 62 SOTHQVSLSKOPTSQSRGDPPTGPK 86

RESULT 3
US-08-450-098-1
Sequence 1, Application US/08450098
Patent No. 5674980
GENERAL INFORMATION:
APPLICANT: FRANKEL, Alan
APPLICANT: PABO, Carl
APPLICANT: BARSOUM, James G.
APPLICANT: FAMELL, Stephen E.
APPLICANT: PEPIISKY, R. B.
TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,098
FILING DATE: 25-MAY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/235,403
FILING DATE: 28-APR-1994
APPLICATION NUMBER: US 07/934,375
FILING DATE: 21-AUG-1992
APPLICATION NUMBER: US 07/098,766
FILING DATE: 28-JUL-1993
APPLICATION NUMBER: PCT/US93/07833
FILING DATE: 19-AUG-1993
APPLICATION NUMBER: US 07/454,450
FILING DATE: 21-DEC-1989
APPLICATION NUMBER: US 07/636,662
FILING DATE: 02-JAN-1991
APPLICATION NUMBER: US 08/158,015
FILING DATE: 24-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B170 CIP 2

```
NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B170 CIP 2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
TELEX: 14-8367
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 86 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: human immunodeficiency virus
STRAIN: type 1
US-08-450-098-1
```

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Query Match          97.7%; Score 465; DB 1; Length 86;
Best Local Similarity 97.6%; Pred. No. 6,4e-45;
Matches 83; Conservative 0; Mismatches 0; Indels 2; Gaps 1;
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Db 2 EPVDPRLPMKHPGSOPTACTNCYCKKCCFHCVCFTTKALGISYGRKKRRRRRPPQG 61
```

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OY 59 SOTHQVSLSKOPTSQSRDPTGPKE 83
    ||||||||||||||||||||||||
Db 62 SOTHQVSLSKOPTSQSRDPTGPKE 86
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RESULT 4

US-08-451-233-1

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; Sequence 1, Application US/08451233
; Patent No. 5747641
; GENERAL INFORMATION:
; APPLICANT: FRANKEL, Alan
; APPLICANT: PABO, Carl
; APPLICANT: BARSOUM, James G.
; APPLICANT: FAWELL, Stephen E.
; APPLICANT: PEPINSKY, R. B.
; TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/451,233
; FILING DATE: 25-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/235,403
; FILING DATE: 28-APR-1994
; APPLICATION NUMBER: US 07/934,375
; FILING DATE: 21-AUG-1992
; APPLICATION NUMBER: US 07/098,766
; FILING DATE: 28-JUL-1993
; APPLICATION NUMBER: PCT/US93/07833
; FILING DATE: 19-AUG-1993
; APPLICATION NUMBER: US 07/454,450
; FILING DATE: 21-DEC-1989
; APPLICATION NUMBER: US 07/636,662
; FILING DATE: 02-JAN-1991
```

```
APPLICATION NUMBER: US 08/158,015
FILING DATE: 24-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B170 CIP 2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
TELEX: 14-8367
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 86 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: human immunodeficiency virus
STRAIN: type 1
US-08-451-233-1
```

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Query Match          97.7%; Score 465; DB 1; Length 86;
Best Local Similarity 97.6%; Pred. No. 6,4e-45;
Matches 83; Conservative 0; Mismatches 0; Indels 2; Gaps 1;
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OY 1 EPVDPRLPMKHPGSOPTACTNCYCKKCCFHCVCFTTKA--ISYGRKKRRRRRPPQG 58
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2 EPVDPRLPMKHPGSOPTACTNCYCKKCCFHCVCFTTKALGISYGRKKRRRRRPPQG 61
```

```
OY 59 SOTHQVSLSKOPTSQSRDPTGPKE 83
    ||||||||||||||||||||||||
Db 62 SOTHQVSLSKOPTSQSRDPTGPKE 86
```

RESULT 5

US-08-450-236-1

```
; Sequence 1, Application US/08450236
; Patent No. 5804604
; GENERAL INFORMATION:
; APPLICANT: FRANKEL, Alan
; APPLICANT: PABO, Carl
; APPLICANT: BARSOUM, James G.
; APPLICANT: FAWELL, Stephen E.
; APPLICANT: PEPINSKY, R. B.
; TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,236
; FILING DATE: 25-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/235,403
; FILING DATE: 28-APR-1994
; APPLICATION NUMBER: US 07/934,375
; FILING DATE: 21-AUG-1992
; APPLICATION NUMBER: US 07/098,766
; FILING DATE: 28-JUL-1993
; APPLICATION NUMBER: PCT/US93/07833
; FILING DATE: 19-AUG-1993
; APPLICATION NUMBER: US 07/454,450
```

FILING DATE: 21-DEC-1989
APPLICATION NUMBER: US 07/636,662
FILING DATE: 02-JAN-1991
APPLICATION NUMBER: US 08/158,015
FILING DATE: 24-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B170 CIP 2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 86 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: human immunodeficiency virus
STRAIN: type 1
US-08-450-236-1

Query Match 97.7%; Score 465; DB 1; Length 86;
Best Local Similarity 97.6%; Pred. No. 6.4e-45;
Matches 83; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 EPVDPRLPEPMKHGSPKPTACTNCYCKCCFHCQVCFITKA--ISYGRKKRRRRRRPPGG 58
|||||
DB 2 EPVDPRLPEPMKHGSPKPTACTNCYCKCCFHCQVCFITKALGISYGRKKRRRRRRPPGG 61
|||||
QY 59 SOTHQVSLSKOPTSOSRGDPTGPKE 83
|||||
DB 62 SOTHQVSLSKOPTSOSRGDPTGPKE 86
|||||

RESULT 6
US-07-808-452-1
Sequence 1, Application US/07808452
Patent No. 6063612
GENERAL INFORMATION:
APPLICANT: Jayasena, Sumedha D.
APPLICANT: Johnston, Brian H.
TITLE OF INVENTION: Antiviral Reagents Based on
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/808,452
FILING DATE: 19911213
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 8255-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:

LENGTH: 86 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: the sequence of the TAR protein of
INDIVIDUAL ISOLATE: HIV-1
US-07-808-452-1

Query Match 97.7%; Score 465; DB 3; Length 86;
Best Local Similarity 97.6%; Pred. No. 6.4e-45;
Matches 83; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 EPVDPRLPEPMKHGSPKPTACTNCYCKCCFHCQVCFITKA--ISYGRKKRRRRRRPPGG 58
|||||
DB 2 EPVDPRLPEPMKHGSPKPTACTNCYCKCCFHCQVCFITKALGISYGRKKRRRRRRPPGG 61
|||||
QY 59 SOTHQVSLSKOPTSOSRGDPTGPKE 83
|||||
DB 62 SOTHQVSLSKOPTSOSRGDPTGPKE 86
|||||

RESULT 7
US-09-030-613-19
Sequence 19, Application US/09030613
Patent No. 6083706
GENERAL INFORMATION:
APPLICANT: Florjanczyk, Robert Z.
APPLICANT: Baird, J. Andrew
TITLE OF INVENTION: INHIBITORS OF LEADERLESS PROTEIN EXPORT
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEDD and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/030,613
FILING DATE: 25-FEB-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: No. 6083706tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 760100.418C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 86 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-030-613-19

Query Match 97.7%; Score 465; DB 3; Length 86;
Best Local Similarity 97.6%; Pred. No. 6.4e-45;
Matches 83; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 EPVDPRLPEPMKHGSPKPTACTNCYCKCCFHCQVCFITKA--ISYGRKKRRRRRRPPGG 58
|||||
DB 2 EPVDPRLPEPMKHGSPKPTACTNCYCKCCFHCQVCFITKALGISYGRKKRRRRRRPPGG 61
|||||

QY 59 SQTHOVSLSKOPTSQSRGDPGPK 83
 Db 62 SQTHOVSLSKOPTSQSRGDPGPK 86

RESULT 8

US-09-124-900-6
 ; Sequence 6, Application US/09124900
 ; Patent No. 6268484
 ; GENERAL INFORMATION:
 ; APPLICANT: KATINGER, Hermann
 ; APPLICANT: BUCHACHER, Andrea
 ; APPLICANT: ERNST, Wolfgang
 ; APPLICANT: BALLAUN, Claudia
 ; APPLICANT: PURTSCHER, Martin
 ; APPLICANT: TRKOJA, Alexandra
 ; APPLICANT: PREDL, Renate
 ; APPLICANT: SCHWATZ, Christine
 ; APPLICANT: KLIMA, Annelies
 ; APPLICANT: STEINDL, Franz
 ; APPLICANT: MUSTER, Thomas
 ; TITLE OF INVENTION: HIV-Vaccines
 ; FILE REFERENCE: 1939-112P
 ; CURRENT APPLICATION NUMBER: US/09/124,900
 ; CURRENT FILING DATE: 1998-07-30
 ; PRIOR APPLICATION NUMBER: PCT/EP95/01481
 ; PRIOR FILING DATE: 1995-04-19
 ; NUMBER OF SEQ ID NOS: 11
 ; SOFTWARE: Patentin version 3.0
 ; SEQ ID NO 6
 ; LENGTH: 86
 ; TYPE: PRF
 ; ORGANISM: Human immunodeficiency virus type 1
 US-09-124-900-6

Query Match 97.7%; Score 465; DB 4; Length 86;
 Best Local Similarity 97.6%; Pred. No. 6.4e-45;
 Matches 83; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 EPVDPRLPEPMKHPGSOPTACTNCTCYKCCCFHCVCFTTKA--ISYGRKKRRRRRRPPG 58
 Db 2 EPVDPRLPEPMKHPGSOPTACTNCTCYKCCCFHCVCFTTKALGISYGRKKRRRRRRPPG 61

QY 59 SQTHOVSLSKOPTSQSRGDPGPK 83
 Db 62 SQTHOVSLSKOPTSQSRGDPGPK 86

RESULT 9

US-09-451-905-19
 ; Sequence 19, Application US/09451905
 ; Patent No. 6306613
 ; GENERAL INFORMATION:
 ; APPLICANT: Robert Z. Florjancic
 ; APPLICANT: Andrew Baird
 ; APPLICANT: Dale E. Wainock
 ; TITLE OF INVENTION: MODULATORS OF LEADERLESS PROTEIN EXPORT
 ; FILE REFERENCE: 200124.402C4
 ; CURRENT APPLICATION NUMBER: US/09/451,905
 ; CURRENT FILING DATE: 1999-12-01
 ; NUMBER OF SEQ ID NOS: 48
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 19
 ; LENGTH: 86
 ; TYPE: PRF
 ; ORGANISM: Homo sapien
 US-09-451-905-19

Query Match 97.7%; Score 465; DB 4; Length 86;

Best Local Similarity 97.6%; Pred. No. 6.4e-45;
 Matches 83; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 EPVDPRLPEPMKHPGSOPTACTNCTCYKCCCFHCVCFTTKA--ISYGRKKRRRRRRPPG 58
 Db 2 EPVDPRLPEPMKHPGSOPTACTNCTCYKCCCFHCVCFTTKALGISYGRKKRRRRRRPPG 61

QY 59 SQTHOVSLSKOPTSQSRGDPGPK 83
 Db 62 SQTHOVSLSKOPTSQSRGDPGPK 86

RESULT 10

PCT-US92-10770-1
 ; Sequence 1, Application PC/TUS9210770
 ; GENERAL INFORMATION:
 ; APPLICANT: Jayasena, Sumedha D.
 ; APPLICANT: Johnston, Brian H.
 ; TITLE OF INVENTION: Antiviral Reagents Based on
 ; -RNA-Binding Proteins
 ; NUMBER OF SEQUENCES: 24
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Sri International
 ; STREET: 333 Ravenswood Avenue
 ; CITY: Menlo Park
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94025
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US92/10770
 ; FILING DATE: 19921211
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/808,452
 ; FILING DATE: 13-DEC-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Fadian, Gary R.
 ; REGISTRATION NUMBER: 33,875
 ; REFERENCE/DOCKET NUMBER: P-2962
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 859-4550
 ; TELEFAX: (415) 859-3880
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 86 amino acids
 ; TYPE: AMINO ACID
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; ORIGINAL SOURCE:
 ; INDIVIDUAL ISOLATE: the sequence of the Tat protein of
 ; HIV-1
 ; PCT-US92-10770-1

Query Match 97.7%; Score 465; DB 5; Length 86;
 Best Local Similarity 97.6%; Pred. No. 6.4e-45;
 Matches 83; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 EPVDPRLPEPMKHPGSOPTACTNCTCYKCCCFHCVCFTTKA--ISYGRKKRRRRRRPPG 58
 Db 2 EPVDPRLPEPMKHPGSOPTACTNCTCYKCCCFHCVCFTTKALGISYGRKKRRRRRRPPG 61

QY 59 SQTHOVSLSKOPTSQSRGDPGPK 83
 Db 62 SQTHOVSLSKOPTSQSRGDPGPK 86

RESULT 11
PCT-US95-06077-2
Sequence 2, Application PC/TUS9506077
GENERAL INFORMATION:
APPLICANT: Immunobiology Research, Institute Inc.
TITLE OF INVENTION: Vaccine Interdiction of Extracellular
TITLE OF INVENTION: Transactivating Proteins of Human Immunodeficiency Virus
TITLE OF INVENTION: and Other Chronically Infecting Viruses Employing Similar
TITLE OF INVENTION: Interellular Transactivating Strategies
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr, PO Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06077
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/247,991
FILING DATE: 23-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 86 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-06077-2

Query Match 97.7%; Score 465; DB 5; Length 86;
Best Local Similarity 97.6%; Pred. No. 6.4e-45;
Matches 83; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 EPVDPRLPEWKHPGSGOPTACTNCTCKKCFHCQVCFITKA--ISYGRKKRRQRRRPPG 58
DB 2 EPVDPRLPEWKHPGSGOPTACTNCTCKKCFHCQVCFITKALGISYGRKKRRQRRRPPG 61

QY 59 SOTHQVLSKOPTSOSRGPDPGPKE 83
DB 62 SOTHQVLSKOPTSOSRGPDPGPKE 86

RESULT 12
US-08-505-210-1
Sequence 1, Application US/08505210
Patent No. 5981258
GENERAL INFORMATION:
APPLICANT: MEHTALI, Majid
APPLICANT: GUSS, Tanja
TITLE OF INVENTION: COMPOSITION OF TRANS-DOMINANT VARIANTS
TITLE OF INVENTION: OF VIRAL PROTEINS FOR OBTAINING AN ANTIVIRAL EFFECT
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
STREET: 1737 King Street, Suite 500
CITY: Alexandria

STATE: Virginia
COUNTRY: United States
ZIP: 22314-2756
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/505,210
FILING DATE: 14-AUG-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,248
FILING DATE: 21-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR94/01457
FILING DATE: 13-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Dadio, Susan M.
REGISTRATION NUMBER: 40,373
REFERENCE/DOCKET NUMBER: 017753-066
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 86 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Human Immunodeficiency virus type 1
STRAIN: Lai
INDIVIDUAL ISOLATE: sequence of the TAT protein of HIV-1
US-08-505-210-1

Query Match 94.3%; Score 449; DB 2; Length 86;
Best Local Similarity 94.1%; Pred. No. 3.9e-43;
Matches 80; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

QY 1 EPVDPRLPEWKHPGSGOPTACTNCTCKKCFHCQVCFITKA--ISYGRKKRRQRRRPPG 58
DB 2 EPVDPRLPEWKHPGSGOPTACTNCTCKKCFHCQVCFITKALGISYGRKKRRQRRRPPG 61

QY 59 SOTHQVLSKOPTSOSRGPDPGPKE 83
DB 62 SOTHQVLSKOPTSOSRGPDPGPKE 86

RESULT 13
US-09-099-333-1
Sequence 1, Application US/09099333A
Patent No. 6228369
GENERAL INFORMATION:
APPLICANT: MEHTALI, Majid
APPLICANT: GUSS, Tanja
TITLE OF INVENTION: COMPOSITION OF TRANS-DOMINANT VARIANTS OF VIRAL
TITLE OF INVENTION: PROTEINS FOR OBTAINING AN ANTI-VIRAL EFFECT
FILE REFERENCE: 017753-091
CURRENT APPLICATION NUMBER: US/09/099,333A
CURRENT FILING DATE: 1998-06-18
EARLIER APPLICATION NUMBER: FR 93 14914
EARLIER FILING DATE: 1993-12-13
EARLIER APPLICATION NUMBER: US 08/215,248
EARLIER FILING DATE: 1994-03-21
EARLIER APPLICATION NUMBER: US 08/505,210
EARLIER FILING DATE: 1995-08-14
NUMBER OF SEQ ID NOS: 7

SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 1
LENGTH: 86
TYPE: PRT
ORGANISM: Human immunodeficiency virus type 1
US-09-099-333-1

Query Match 94.3%; Score 449; DB 4; Length 86;
Best Local Similarity 94.1%; Pred. No. 3.9e-43;
Matches 80; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

QY 1 EPVDPRLPEPKHSGSPKTAICTNCYCKCCFHCQVCFTKA--ISYGRKKRRQRRRPPQG 58
|||||
DB 2 EPVDPRLPEPKHSGSPKTAICTNCYCKCCFHCQVCFTKALGISTYGRKKRRQRRRPPQG 61
|||||
QY 59 SOTHQVSLSKOPTSOSRGDPTGPK 83
|||||
DB 62 SOTHQVSLSKOPTSOSRGDPTGPK 86

RESULT 14
US-08-053-079A-15
Sequence 15, Application US/08053079A
Patent No. 5606026
GENERAL INFORMATION:
APPLICANT: Rodman
TITLE OF INVENTION: Natural Human Igm Antibodies
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby
STREET: 805 Third Ave.
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/053,079A
FILING DATE: 26-APR-1993
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Robinson, Joseph, R.
REGISTRATION NUMBER: 33,448
REFERENCE/DOCKET NUMBER: 4436/16060US4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)527-7700
TELEFAX: (212)753-6237
TELEX: 236687
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 82
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-053-079A-15

Query Match 91.2%; Score 434; DB 1; Length 82;
Best Local Similarity 96.3%; Pred. No. 1.7e-41;
Matches 78; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

QY 1 EPVDPRLPEPKHSGSPKTAICTNCYCKCCFHCQVCFTKA--ISYGRKKRRQRRRPPQG 58
|||||
DB 2 EPVDPRLPEPKHSGSPKTAICTNCYCKCCFHCQVCFTKALGISTYGRKKRRQRRRPPQE 61
|||||
QY 59 SOTHQVSLSKOPTSOSRGDPT 79
|||||
DB 62 SOTHQVSLSKOPTSOSRGDPT 82

RESULT 15
US-09-030-613-17
Sequence 17, Application US/09030613
Patent No. 6083706
GENERAL INFORMATION:
APPLICANT: Florkiewicz, Robert Z.
APPLICANT: Baird, J. Andrew
TITLE OF INVENTION: INHIBITORS OF LEADERLESS PROTEIN EXPORT
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/030,613
FILING DATE: 25-FEB-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: NO. 6083706tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 760100.418C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 72 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-030-613-17

Query Match 81.5%; Score 388; DB 3; Length 72;
Best Local Similarity 97.2%; Pred. No. 1.9e-36;
Matches 69; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 EPVDPRLPEPKHSGSPKTAICTNCYCKCCFHCQVCFTKA--ISYGRKKRRQRRRPPQG 58
|||||
DB 2 EPVDPRLPEPKHSGSPKTAICTNCYCKCCFHCQVCFTKALGISTYGRKKRRQRRRPPQG 61
|||||
QY 59 SOTHQVSLSKO 69
|||||
DB 62 SOTHQVSLSKO 72

Search completed: January 10, 2002, 15:35:15
Job time: 73 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 10, 2002, 15:34:02 ; Search time 14.89 Seconds

(without alignments)
424.613 Million cell updates/sec

Title: US-09-555-534-2

Perfect score: 476
Sequence: 1 EPVDPRLPMPKHPGSGPRTA.....VSLSKOPTSOSRGDPGPKE 83

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : PIR_68:*

1: p1r1:*

2: p1r2:*

3: p1r3:*

4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	465	97.7	86	2 S33982	trans-activating t
2	457	96.0	95	1 TNLJ12	trans-activating t
3	449	94.3	86	2 A25700	trans-activating t
4	415	87.2	101	2 T09446	fat protein - huma
5	412	86.6	101	1 E44001	trans-activating t
6	390	81.9	86	2 JC5591	transactivator pro
7	387	81.3	86	2 S54381	fat protein - huma
8	384	80.7	86	1 TNLJZR	trans-activating t
9	382	80.3	86	1 TNLJND	trans-activating t
10	374.5	78.7	87	2 T01655	fat protein - huma
11	344	72.3	72	1 TNLJH4	trans-activating t
12	333	70.0	71	2 T09384	trans-activating t
13	297.5	62.5	100	1 TNLJST	trans-activating t
14	165.5	34.8	130	1 TNLJGC	trans-activating t
15	160.5	33.7	130	1 TNLJST	trans-activating t
16	160.5	33.7	130	2 S53096	fat protein - huma
17	149	31.3	130	2 S12157	trans-activating t
18	148.5	31.2	130	1 TNLJG2	trans-activating t
19	148	31.1	133	1 TNLJCA	trans-activating t
20	141.5	29.7	129	1 TNLJG3	trans-activating t
21	139.5	29.3	106	1 TNLJG2	trans-activating t
22	133.5	28.0	96	2 S08440	trans-activating t
23	126.5	26.6	132	2 T11564	fat protein - siml
24	122	25.6	100	1 TNLJG4	trans-activating t
25	122	25.6	119	2 A46356	fat protein - siml
26	120	25.2	131	2 T11557	fat protein - siml
27	112.5	23.6	116	1 A48344	trans-activating t
28	106	22.3	73	2 S46349	trans-activating t
29	101.5	21.3	145	1 TNLJBT	trans-activating t

30	77.5	16.3	346	2 P96785	protein F10A5.26 l
31	76	16.0	171	1 BG802	spermatid transiti
32	76	16.0	134	2 G84600	hypothetical prote
33	76	16.0	390	2 I51419	transcription fact
34	74	15.5	388	2 I51420	transcription fact
35	73.5	15.4	1477	2 T13797	tumor suppressor pr
36	72.5	15.2	222	2 E84560	hypothetical prote
37	72	15.1	137	1 BGP62	spermatid transiti
38	70.5	14.8	3942	2 T42730	Bassoon protein -
39	70	14.7	477	2 T23554	hypothetical prote
40	69.5	14.6	159	2 J00145	hypothetical 17.3k
41	69.5	14.6	1138	2 S64484	phosphatidylserine
42	69	14.5	322	2 T04595	hypothetical prote
43	69	14.5	3198	2 A43426	collagen alpha 2 f
44	68	14.3	944	1 S48821	probable membrane
45	67.5	14.2	895	2 T02597	Mutator-like trans

ALIGNMENTS

```
RESULT 1
S33982      trans-activating transcription regulator - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C>Date: 06-Oct-1994 #sequence_revision 23-Feb-1996 #text_change 20-Sep-1999
C:Accession: S33982; S26385; S19664
R:Carlini, F.
Submitted to the EMBL Data Library, November 1991
A:Reference number: S33979
A:Accession: S33982
A:Molecule-type: DNA
A:Residues: 1-86 <CAR>
A:Cross-references: EMBL:11530; NID:960192; PIDN:CAA77625.1; PID:960196
R:Slidrovski, D.P.; Matsuyama, T.; Figerio, E.; Chui, S.; Min, X.; Effle, H.; Summer
Nucleic Acids Res. 20, 5311-5320, 1992
A>Title: Random mutagenesis of the human immunodeficiency virus type-1 trans-actvato
A:Reference number: S26385; MUID:93065196
A:Accession: S26385
A:Molecule type: nucleic acid
A:Residues: 1-86 <STD>
A:Cross-references: EMBL:X64650; NID:960144; PIDN:CAA5921.1; PID:960145
C:Genetics:
A:Gene: tat
A:Introns: 72/2
C:Superfamily: AIDS trans-activating transcription regulator
C:Keywords: AIDS; Immunodeficiency

Query Match      97.7%; Score 465; DB 2; Length 86;
Best local Similarity 97.6%; Pred. No. 1, 2e-38;
Matches 83; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

OY 1 EPVDPRLPMPKHPGSGPRTACTNCYCKCCFHCQVCEPTKA--ISYGRKKRRQRRRPQG 58
    |||||||
Db 2 EPVDPRLPMPKHPGSGPRTACTNCYCKCCFHCQVCEPTKAIGSYGRKKRRQRRRPQG 61
    |||||||

OY 59 SOTHVSLSKOPTSOSRGDPGPKE 83
    |||||||
Db 62 SOTHVSLSKOPTSOSRGDPGPKE 86
    |||||||

RESULT 2
TNLJ12      trans-activating transcription regulator - human immunodeficiency virus type 1 (isola
C:Species: human immunodeficiency virus type 1, HIV-1
A>Note: host Homo sapiens (man)
C>Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 02-Jul-1998
C:Accession: A04017
R:Arya, S.K.; Gallo, R.C.
Proc. Natl. Acad. Sci. U.S.A. 83, 2209-2213, 1986
A>Title: Three novel genes of human T-lymphotropic virus type III: immune reactivity
A:Reference number: A94093; MUID:86177573
```


A:Accession: F33943
A:Molecule type: genomic RNA
A:Residues: 1-130 <KUM>
A:Cross-References: GB:M31113; NID:g1339798; PIDN:AAB01356.1; PID:g325753
C:Genetics:
A:Gene: tat
A:Introns: 99/2
C:Superfamily: AIDS trans-activating transcription regulator
C:Keywords: transcription

Query Match 33.7%; Score 160.5; DB 1; Length 130;
Best Local Similarity 40.6%; Pred. No. 7.2e-09;
Matches 28; Conservative 14; Mismatches 26; Indels 1; Gaps 1;
QY 16 OPTACTN-CYCKKCCFHQVCFITKAISYGRKKRRRRRPPQGSQTHQVSLSKOPTSQS 74
DB 45 QPLEACDNKCYCKKCCYHCQMCFLNKGIGIWTYERKGRRRRPFKTKAHSSASDKSISTR 104
QY 75 RGDPTGPKE 83
DB 105 TGNSSQPEKK 113

Search completed: January 10, 2002, 15:34:56
Job time: 54 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 10, 2002, 15:34:02 ; Search time 11.72 Seconds

(without alignments)
259,657 Million cell updates/sec

Title: US-09-555-534-2

Perfect score: 476
Sequence: 1 EPVDRLEPMKHNPGSQPKTA.....VSLSKPTSGSGDPTGPK 83

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	465	97.7	86	TAT_HV1B1	P04606 human immun
2	460	96.6	86	TAT_HV1P	P04607 human immun
3	457	96.0	86	TAT_HV112	P04336 human immun
4	449	94.3	86	TAT_HV1BR	P04610 human immun
5	439	92.2	102	TAT_HV1RH	P05908 human immun
6	433	91.0	86	TAT_HV1H2	P04608 human immun
7	424	89.1	101	TAT_HV1JR	P20879 human immun
8	415	87.2	101	TAT_HV1SC	P05906 human immun
9	414	87.0	101	TAT_HV1C4	P05907 human immun
10	413	86.8	101	TAT_HV1S1	P19563 human immun
11	412	86.6	101	TAT_HV1Y2	P35965 human immun
12	409	85.9	101	TAT_HV1MN	P05905 human immun
13	409	85.9	101	TAT_HV1S3	P19552 human immun
14	397	83.4	101	TAT_HV1A2	P04614 human immun
15	397	83.4	101	TAT_HV1OY	P20893 human immun
16	387	81.3	86	TAT_HV1Z2	P12506 human immun
17	384	80.7	86	TAT_HV1Z6	P04609 human immun
18	382	80.3	86	TAT_HV1ND	P18804 human immun
19	374.5	78.7	87	TAT_HV1MA	P04613 human immun
20	371	77.9	99	TAT_HV1E4	P04611 human immun
21	320	67.2	101	TAT_HV1U4	P24738 human immun
22	304	63.9	58	TAT_HV1B5	P04612 human immun
23	297.5	62.5	100	TAT_HV1C2	P17285 chimpanzee
24	165.5	34.8	130	TAT_HV2G1	P18044 human immun
25	160.5	33.7	130	TAT_HV2ST	P20880 human immun
26	159.5	33.5	130	TAT_HV2KR	P04614 human immun
27	150.5	31.6	130	TAT_HV1M1	P05911 simian immun
28	149	31.3	130	TAT_HV2D1	P17759 human immun
29	148.5	31.2	130	TAT_HV2RO	P04605 human immun
30	148	31.1	133	TAT_HV2CA	P24109 human immun
31	147.5	31.0	130	TAT_HV2NE	P18098 human immun
32	145	30.5	130	TAT_HV2BZ	P05909 human immun
33	139.5	29.3	106	TAT_HV1WL	P11263 simian immun

ALIGNMENTS

RESULT	ID	STANDARD	PRT	86 AA
1	TAT_HV1B1			
AC	P04606			
DT	13-AUG-1987 (Rel. 05, Created)			
DT	13-AUG-1987 (Rel. 05, Last sequence update)			
DT	20-AUG-2001 (Rel. 40, Last annotation update)			
DE	TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).			
OS	Human immunodeficiency virus type 1 (BH10 isolate) (HIV-1), and			
OS	Human immunodeficiency virus type 1 (HXB3 isolate) (HIV-1).			
OC	Viruses; Retroviridae; Retroviridae; Lentivirus.			
OX	NCBI_TaxID=11678, 11707;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-ISOLATE BH10;			
RC	MEDLINE=85111123; Pubmed=2578615;			
RA	Ratner L., Haseltine W., Patarca R., Livak K.J., Starcich B.R.,			
RA	Josephus S.F., Doran E.R., Ratajski J.A., Whitehorn E.A.,			
RA	Baumelster K., Ivanoff L., Petteway S.R. Jr., Pearson M.L.,			
RA	Lautenberger J.A., Papas T.S., Graybe J., Chang N.T., Gallo R.C.,			
RA	Wong-Staal F.;			
RT	"Complete nucleotide sequence of the AIDS virus, HTLV-III.";			
RL	Nature 313:277-284(1985).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-ISOLATE HXB3;			
RC	MEDLINE=85228248; Pubmed=2988795;			
RX	Crowl R., Ganguly K., Gordon M., Conroy R., Schaber M., Kramer R.,			
RA	Shaw G.M., Wong-Staal F., Reddy E.P.;			
RT	"HTLV-III env gene products synthesized in E. coli are recognized by			
RT	antibodies present in the sera of AIDS patients.";			
RL	Cell 41:979-986(1985).			
CC	-1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE			
CC	TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND			
CC	ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR			
CC	PROMOTER.			
CC	-1- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).			
CC	-1- SUBCELLULAR LOCATION: NUCLEAR; NUCLEAR.			
CC	-1- MISCELLANEOUS: THE TWO ISOLATES TAR SEQUENCE ARE IDENTICAL.			
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CC	or send an email to license@sib-sib.ch).			
CC	-----			
CC	EMBL; M14100; AAA44676.1; -			P12453 human immun
DR	EMBL; M15654; AAA44199.1; -			P05910 simian immun
DR	HIV; M15654; TATSH102.			O02838 simian immun
DR	HIV; M14100; TATSHXB3.			P15835 human immun
DR	InterPro: IP001831; HIV_Tat.			P19507 simian immun
DR	Pfam: PF00539; Tat_1			P12513 simian immun
DR	PRINTS; PR00055; HIVTANOMAIN.			P27975 simian immun
DR				P05913 simian immun
DR				P27982 simian immun
DR				P12507 simian immun
DR				P22384 simian immun
DR				P36340 simian immun

KW Transcription regulation; Activator; RNA-binding; Nuclear protein;
 KW AIDS.
 SO SEQUENCE 86 AA: 9784 MW: 4DD609415FAF9015 CRC64;

Query Match 97.7%; Score 465; DB 1; Length 86;
 Best Local Similarity 97.6%; Pred. No. 2e-41;
 Matches 83; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

OY 1 EVDPRLEPMKHPGSOPTACTNCCCKCCFHCQVCFITKA--TSYGRKKRRRRRRPPQG 58
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 2 EVDPRLEPMKHPGSOPTACTNCCCKCCFHCQVCFITKALGISYGRKKRRRRRRPPQG 61
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 OY 59 SOTHQVSLSKOPTSOSRGDPTGPKE 83
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 62 SOTHQVSLSKOPTSOSRGDPTGPKE 86

RESULT 2

TAT_HV1PV STANDARD; PRT; 86 AA.
 AC P04607;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).
 GN TAT.
 OS Human immunodeficiency virus type 1 (PV22 isolate) (HIV-1).
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_Taxid=11700;
 RN MEDLINE=8511157; PubMed=2982104;
 RX Muesing M.A., Smith D.H., Cabradilla C.D., Benton C.V., Lasky L.A.,
 RA Capon D.J.;
 RT "Nucleic acid structure and expression of the human
 RT Aids/Lymphadenopathy retrovirus.";
 RL Nature 313:450-458(1985).
 CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
 CC -1- TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
 CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
 CC PROMOTER.
 CC -1- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
 CC CC
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 CC
 CC EMBL: K02083; AAB59870.1; -;
 DR EMBL: X01762; -; NOT_ANNOTATED_CDS.
 DR HIV: K02083; TATSPV22.
 DR InterPro: IPR001831; HIV_Tat.
 DR Pfam: PF00539; Tat.1.
 DR PRINTS: PR00055; HIVTATDOMAIN.
 DR Transcription regulation; Activator; RNA-binding; Nuclear protein;
 KW AIDS.
 SO SEQUENCE 86 AA: 9794 MW: 4DD5C6415FAF9015 CRC64;

Query Match 96.6%; Score 460; DB 1; Length 86;
 Best Local Similarity 96.5%; Pred. No. 6.5e-41;
 Matches 82; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

OY 1 EVDPRLEPMKHPGSOPTACTNCCCKCCFHCQVCFITKA--TSYGRKKRRRRRRPPQG 58
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 2 EVDPRLEPMKHPGSOPTACTNCCCKCCFHCQVCFITKALGISYGRKKRRRRRRPPQG 61
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 OY 59 SOTHQVSLSKOPTSOSRGDPTGPKE 83

DB 62 SOTHQVSLSKOPTSOSRGDPTGPKE 86
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

RESULT 3

TAT_HV112 STANDARD; PRT; 86 AA.
 AC P04326;
 DT 20-MAR-1987 (Rel. 04, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).
 GN TAT.
 OS Human immunodeficiency virus type 1 (clone 12) (HIV-1).
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_Taxid=11679;
 RN MEDLINE=8617573; PubMed=3008154;
 RX Arya S.K., Gallo R.C.;
 RA "Three novel genes of human T-lymphotropic virus type III: Immune
 RT reactivity of their products with sera from acquired immune
 RT deficiency syndrome patients.";
 RT Proc. Natl. Acad. Sci. U.S.A. 83:2209-2213(1986).
 CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
 CC -1- TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
 CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
 CC PROMOTER.
 CC -1- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
 CC CC
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 CC
 CC EMBL: M11840; AAA44999.1; -;
 DR EMBL: M11840; TNLJ12.
 DR HIV: M11840; TATSPV12.
 DR InterPro: IPR001831; HIV_Tat.
 DR Pfam: PF00539; Tat.1.
 DR PRINTS: PR00055; HIVTATDOMAIN.
 DR Transcription regulation; Activator; RNA-binding; Nuclear protein;
 KW AIDS.
 SO SEQUENCE 86 AA: 9758 MW: 4DD609414FBE9115 CRC64;

Query Match 96.0%; Score 457; DB 1; Length 86;
 Best Local Similarity 96.5%; Pred. No. 1.3e-40;
 Matches 82; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

OY 1 EVDPRLEPMKHPGSOPTACTNCCCKCCFHCQVCFITKA--TSYGRKKRRRRRRPPQG 58
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 2 EVDPRLEPMKHPGSOPTACTNCCCKCCFHCQVCFITKALGISYGRKKRRRRRRPPQG 61
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 OY 59 SOTHQVSLSKOPTSOSRGDPTGPKE 83
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 62 SOTHQVSLSKOPTSOSRGDPTGPKE 86

RESULT 4

TAT_HV1BR STANDARD; PRT; 86 AA.
 AC P04610;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).
 GN TAT.
 OS Human immunodeficiency virus type 1 (BRU isolate) (HIV-1).

OC Viruses; Retroïd viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11686;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85099333; PubMed=2981635;
 RA Wain-Hobson S.; Sonigo P.; Danos O.; Cole S.; Alizon M.;
 RT "Nucleotide sequence of the AIDS virus, LAV";
 RL Cell 40:9-17(1985).
 RN [2]
 RP SEQUENCE FROM N.A. (CLONE PNL4-3).
 RA Buckler C.E., Buckler-White A.J., Willey R.L., McCoy J.;
 RL Submitted (JUN-1988) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
 CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
 CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
 CC PROMOTER.
 CC -1- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
 CC -----
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 CC -----
 CC EMBL: K02013; AAB59745.1; -;
 DR EMBL: M19921; AAA44985.1; -;
 DR HIV: K02013; TATSRU.
 DR HIV: M19921; TATSNL43.
 DR InterPro: IPR001831; HIV_Tat.
 DR Pfam: PF00539; Tat; 1.
 DR PRINTS: PR00055; HIVTATDOMAIN.
 KM Transcription regulation; Activator; RNA-binding; Nuclear protein;
 KW AIDS.
 FT VARIANT 24 24 T -> N (IN CLONE PNL4-3).
 FT VARIANT 39 39 T -> M (IN CLONE PNL4-3).
 FT VARIANT 58 61 PPOG -> AHON (IN CLONE PNL4-3).
 FT VARIANT 67 67 V -> A (IN CLONE PNL4-3).
 FT VARIANT 77 77 P -> S (IN CLONE PNL4-3).
 SQ SEQUENCE 86 AA; 9769 MW; 9B1BA915FAF8A14 CRC64;

Query Match 94.3%; Score 449; DB 1; Length 86;
 Best Local Similarity 94.1%; Pred. No. 8.7e-40;
 Matches 80; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

QY 1 EPVDPRLPEPKHPSQPTACTNCYCKKCCFHCQVCFITK--ISYGRKKRRORRRPPOG 58
 |||||||
 DB 2 EPVDPRLPEPKHPSQPTACTNCYCKKCCFHCQVCFITKALGISYGRKKRRORRRPPOG 61
 |||||||
 QY 59 SOTHQVSLSKOPTSOSRGDPTGPK 83
 |||||||
 DB 62 SQTHQVSLSKOPTSOSRGDPTGPK 86
 |||||||

RESULT 5
 TAT_HV1RH STANDARD; PRT; 102 AA.
 ID TAT_HV1RH
 AC P05908;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).
 GN TAT.
 OS Human immunodeficiency virus type 1 (HF/HAT isolate) (HIV-1).
 OC Viruses; Retroïd viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11701;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86218077; PubMed=2423250;
 RA Starcich B.R.; Hahn B.H.; Shaw G.M.; McNeely P.D.; Modrow S.;

RA Wolf H., Parks E.S., Parks W.P., Josephs S.F., Gallo R.C.,
 RA Wong-Staal F.;
 RT "Identification and characterization of conserved and variable
 RT regions in the envelope gene of HTLV-III/LAV, the retrovirus of
 RT AIDS";
 RL Cell 45:637-648(1986).
 CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
 CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
 CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
 CC PROMOTER.
 CC -1- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
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 CC -----
 CC EMBL: M17451; TATSRF.
 DR HIV: M17451; TATSRF.
 DR InterPro: IPR001831; HIV_Tat.
 DR Pfam: PF00539; Tat; 1.
 DR PRINTS: PR00055; HIVTATDOMAIN.
 KM Transcription regulation; Activator; RNA-binding; Nuclear protein;
 KW AIDS.
 SQ SEQUENCE 102 AA; 11538 MW; 3EACFB843C5195BD CRC64;

Query Match 92.2%; Score 439; DB 1; Length 102;
 Best Local Similarity 90.6%; Pred. No. 1.1e-38;
 Matches 77; Conservative 2; Mismatches 4; Indels 2; Gaps 1;

QY 1 EPVDPRLPEPKHPSQPTACTNCYCKKCCFHCQVCFITK--AISYGRKKRRORRRPPOG 58
 |||||||
 DB 2 EPVDPRLPEPKHPSQPTACTNCYCKKCCFHCQVCFITKALGISYGRKKRRORRRPPOG 61
 |||||||
 QY 59 SOTHQVSLSKOPTSOSRGDPTGPK 83
 |||||||
 DB 62 SQTHQVSLSKOPTSOSRGDPTGPK 86
 |||||||

RESULT 6
 TAT_HV1H2 STANDARD; PRT; 86 AA.
 ID TAT_HV1H2
 AC P04608; 009778;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).
 GN TAT.
 OS Human immunodeficiency virus type 1 (HXB2 isolate) (HIV-1).
 OC Viruses; Retroïd viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11706;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=8729196; PubMed=3040055;
 RA Ratner L., Fisher A., Jagodzinski L.L., Mitsuya H., Liou R.-S.,
 RA Gallo R.C., Wong-Staal F.;
 RT "Complete nucleotide sequences of functional clones of the AIDS
 RT virus";
 RL AIDS Res. Hum. Retroviruses 3:57-69(1987).
 RN [2]
 RP REVISIONS.
 RA Ratner L., Fisher A., Jagodzinski L.L., Mitsuya H., Liou R.-S.,
 RA Gallo R.C., Wong-Staal F.;
 RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
 CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
 CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
 CC PROMOTER.

CC -1- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: K03455; AAB50256.1; -
DR EMBL: AF033819; AAC82591.1; -
DR HIV: K03455; TATSHXB2
DR InterPro: IPR001831; HIV_Tat.
DR Pfam: PF00539; Tat; 1.
DR PRINTS: PR00055; HIVTATDOMAIN.
KW Transcription regulation; Activator; RNA-binding; Nuclear protein;
KW AIDS.
SQ SEQUENCE 86 AA: 9837 MW: 4DDC56D979769115 CRC64;

Query Match 91.0%; Score 433; DB 1; Length 86;
Best Local Similarity 91.8%; Pred. No. 3.8e-38;
Matches 78; Conservative 0; Mismatches 5; Indels 2; Gaps 1;

OY 1 EVDVRLPEWKHPGSGOPTACTNCTCKKCCFHCQVCFITK--AISYGRKKRRRRPPQG 58
Db 2 EVDVRLPEWKHPGSGOPTACTNCTCKKCCFHCQVCFITKALGISYGRKKRRRRPPQD 61
OY 59 SOTHQVSLSKOPTSQRGDPPTGPK 83
Db 62 SOTHQVSLSKOPTSQRGDPPTGPK 86

RESULT 7
TAT_HV1JR STANDARD; PRT; 101 AA.
AC P20879;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).
GN TAT.
OS Human immunodeficiency virus type 1 (JRCSF isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11688;
RN [1]
RP SEQUENCE FROM N.A.
RA Koyanagi S., Chen I.S.Y.;
RA Submitted (Dec-1988) to the HIV data bank.
CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER.
CC -1- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M38429; -; NOT_ANNOTATED_CDS.
DR HIV: M38429; TATSRCSF.
DR InterPro: IPR001831; HIV_Tat.
DR Pfam: PF00539; Tat; 1.
DR PRINTS: PR00055; HIVTATDOMAIN.
KW Transcription regulation; Activator; RNA-binding; Nuclear protein;
KW AIDS.

SQ SEQUENCE 101 AA: 11508 MW: 3E6C8D8FF7F8D4FA CRC64;

Query Match 89.1%; Score 424; DB 1; Length 101;
Best Local Similarity 88.2%; Pred. No. 3.7e-37;
Matches 75; Conservative 1; Mismatches 7; Indels 2; Gaps 1;

OY 1 EVDVRLPEWKHPGSGOPTACTNCTCKKCCFHCQVCFITK--AISYGRKKRRRRPPQG 58
Db 2 EVDVRLPEWKHPGSGOPTACTNCTCKKCCFHCQVCFITKALGISYGRKKRRRRPPQD 61
OY 59 SOTHQVSLSKOPTSQRGDPPTGPK 83
Db 62 SOTHQVSLSKOPTSQRGDPPTGPK 86

RESULT 8
TAT_HV1SC STANDARD; PRT; 101 AA.
ID TAT_HV1SC
AC P05906;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).
GN TAT.
OS Human immunodeficiency virus type 1 (SC isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11702;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=88219542; PubMed=3369091;
RX Gurgu C., Guo H.-G., Franchini G., Aldovini A., Collalti E.,
RA Farrell K., Wong-Staal F., Gallo R.C., Reitz M.S. Jr.;
RT "Envelope sequences of two new United States HIV-1 isolates";
RL Virology 164:531-536(1988).
CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER.
CC -1- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
CC -1- MISCELLANEOUS: THE SC ISOLATE WAS TAKEN FROM AN ARC PATIENT IN
CC 1984 IN SOUTHERN CALIFORNIA.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M17450; AAA45060.1; -
DR HIV: M17450; TAT5SC.
DR InterPro: IPR001831; HIV_Tat.
DR Pfam: PF00539; Tat; 1.
DR PRINTS: PR00055; HIVTATDOMAIN.
KW Transcription regulation; Activator; RNA-binding; Nuclear protein;
KW AIDS.
SQ SEQUENCE 101 AA: 11426 MW: C9109B938D15788 CRC64;

Query Match 87.2%; Score 415; DB 1; Length 101;
Best Local Similarity 85.9%; Pred. No. 3.1e-36;
Matches 73; Conservative 3; Mismatches 7; Indels 2; Gaps 1;

OY 1 EVDVRLPEWKHPGSGOPTACTNCTCKKCCFHCQVCFITK--AISYGRKKRRRRPPQG 58
Db 2 EVDVRLPEWKHPGSGOPTACTNCTCKKCCFHCQVCFITKALGISYGRKKRRRRPPQD 61
OY 59 SOTHQVSLSKOPTSQRGDPPTGPK 83
Db 62 SOTHQVSLSKOPTSQRGDPPTGPK 86

```
RESULT 9
RN TAT_HV1C4
ID TAT_HV1C4 STANDARD; PRT; 101 AA.
AC P05907;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE TAT PROTEIN (TRANSACTIVATING REGULATOR PROTEIN).
GN TAT.
OS Human immunodeficiency virus type 1 (CDC-451 isolate) (HIV-1).
OC Viruses; Retrovirdae; Lentiviridae; Lentivirus.
NCBI_TaxID=11687;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87041461; Pubmed=3490666;
RA Desai S.M., Kalyanaraman V.S., Casey J.M., Srinivasan A.,
RA Andersen P.R., Devare S.G.;
RT "Molecular cloning and primary nucleotide sequence analysis of a
RT distinct human immunodeficiency virus isolate reveal significant
RT divergence in its genomic sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:8380-8384(1986)
CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER.
CC -1- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M13137; AAA44309.1; -.
DR PIR: B25523; TNLJH4.
DR HIV: M13137; TATSCD45.
DR InterPro: IPR001831; HIV_Tat.
DR Pfam: PF00539; Tat; 1.
DR PRINTS: PR00055; HIVTATDOMAIN.
KM Transcription regulation; Activator; RNA-binding; Nuclear protein;
KM AIDS.
SQ SEQUENCE 101 AA; 11594 MW; 817D915F3FB1C7FA CRC64;
```

```
OX NCBI_TaxID=11691;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90347835; Pubmed=2384920;
RA Cheng-Mayer C., Quiroga M., Tung J.W., Dina D., Levy J.,
RT "Viral determinants of human immunodeficiency virus type 1 T-cell or
RT macrophage tropism, cytopathogenicity, and CD4 antigen modulation.";
RL J. Virol. 64:4390-4398(1990).
CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER.
CC -1- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M65024; AAA5069.1; -.
DR HIV: M38428; TATSEF162.
DR InterPro: IPR001831; HIV_Tat.
DR Pfam: PF00539; Tat; 1.
DR PRINTS: PR00055; HIVTATDOMAIN.
KM Transcription regulation; Activator; RNA-binding; Nuclear protein;
KM AIDS..
SQ SEQUENCE 101 AA; 11497 MW; 8CE2C48C263293C CRC64;
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Query Match 86.8%; Score 413; DB 1; Length 101;
Best Local Similarity 85.9%; Pred. No. 5e-36;
Matches 73; Conservative 2; Mismatches 8; Indels 2; Gaps 1;

```
QY 1 EPVDPRLPEPKHPSQPTACTNCTCKKCFHCVCFTTK--AISYGRKKRRRRRPPG 58
    |||||
DB 2 EPVDPRLPEPKHPSQPTACTNCTCKKCFHCVCFTTGLGISYGRKKRRRRRPPD 61
    |||||
QY 59 SQTHQVSLSKOPTSQSRGDDPTGPKE 83
    |||||
DB 62 SEVHQVSLKOPASQSRGDDPTGPKE 86
    |||||
```

RESULT 11
TAT_HV1Y2
ID TAT_HV1Y2 STANDARD; PRT; 101 AA.
AC P35965;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE TAT PROTEIN (TRANSACTIVATING REGULATOR PROTEIN).
GN TAT.
OS Human immunodeficiency virus type 1 (YU-2 isolate) (HIV-1).
OC Viruses; Retrovirdae; Lentiviridae; Lentivirus.
NCBI_TaxID=36377;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93021387; Pubmed=1404605;
RA Li Y., Hui H., Burgess C.J., Price R.W., Sharp P.M., Hahn B.H.,
RA Shaw G.M.;
RT "Complete nucleotide sequence, genome organization, and biological
RT properties of human immunodeficiency virus type 1 in vivo: evidence
RT for limited defectiveness and complementation.";
RL J. Virol. 66:6587-6600(1992).
CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER.
CC -1- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.

	Query Match	86.6%	Score 412	DB 1	Length 101
	Best Local Similarity	85.9%	Pred. No. 6.3e-36		
	Matches 73	Conservative 1	Mismatches 9	Indels 2	Gaps 1
Qy	1	EPVDRLPEWKRHPGSGPACTNCYCKKCCFCAQCYCFITK--ALSYGRRKRRORRRPQG	58		
Db	2	EPVDNLELWKRHPGSGPACTNCCYCKKCCFCAQCYCFITKGLGISYGRKKRRORRRPQD	61		
Qy	59	SOTHOSSLKOPTSOSRGDPTGPK	83		
Db	62	SOTHOSSLKOPTSOLRGDPTGPT	86		

Query Match	Best Local Similarity	Matches	Score	DB	Length	Indels	Gaps
85.9%	85.9%	1	409	1	101	2	1
Transcription regulation; Activator; RNA-binding; Nuclear protein; AIDS.	101 AA; 11634 MM; 2DBC7A21486389FF CRC64	73; Conservative	Pred. No. 1.3e-35;				
1	EPVDRLEPMWHPGSOPTACTNCYCKKCCFHCQVCFITKA--ISYGRKKRRORRRRPOG	58					
2	EEVDRLPELWKPWGSOPTACTTCYCKKCCFHCQVCFITKALGISYGRKKRRORRRRAED	61					
59	SQTHQVSLSKOPTSOSRGPPTGPKK	83					
62	SQTHQVSLSKOPTSOSRGPPTGPKK	86					

ID	TAT_HV153	STANDARD:	PRT:	101 AA.
DT	01-FEB-1991	(Rel. 17, Created)		
DT	01-FEB-1991	(Rel. 17, Last sequence update)		
DT	20-AUG-2001	(Rel. 40, Last annotation update)		
DE	TAT PROTEIN	(TRANSACTIONAL REGULATORY PROTEIN).		
GN	TAT			
OC	Human immunodeficiency virus type 1 (SF3 isolate) (HIV-1).			
OC	Viruses; Retroid viruses; Retroviridae; Lentivirus.			
OX	NCBI_TaxID=11690;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=90317906; Pubmed=2370688;			
RA	Yoriz-Higgins D., Cheng-Mayer C., Bauer D., Levy J.A., Dina D.;			
RT	"Human immunodeficiency virus type 1 cellular host range,			
RT	replication, and cytopathicity are linked to the envelope region of			
RL	the viral genome.";			
CC	J. Virol. 64:4016-4020(1990).			
CC	-1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE			
CC	TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND			
CC	ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR			
CC	PROMOTER.			
CC	-1- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).			
CC	-1- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.			
CC	-----			
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CC	or send an email to license@isb-sib.ch).			
DR	EMBL: M38427; -; NOT_ANNOTATED_CDS.			
DR	HIV: M38427; TATSF33.			
DR	InterPro: IPR001831; HIV_Tat.			
DR	Pfam: PF00539; Tat; 1.			
DR	PRINTS: PRO0055; HIVTATDOMAIN.			
KW	Transcription regulation; Activator; RNA-binding; Nuclear protein;			
AIDS.				
KW	SEQUENCE: 101 AA; 11502 MW; 28C830FF3287970A CRC64;			
QY	Query Match	85.9%;	Score 409;	DB 1; Length 101;
Db	Best Local Similarity	84.7%;	Pred. No. 1.3e-35;	
Matches	72; Conservative	3;	Mismatches	8; Indels 2; Gaps 1.
QY	1 EPVDPRLPEPKHFGSOPKTACTNCYCKCCFHCVCPEITK--AISTGKRRKRORRRPPG	58		
Db	2 EPVDPRLPEPKHFGSOPKTACTNCYCKCCFHCVCPEITKGLTGLTSGKRRKRORRRPPG	61		
QY	59 SOTHOVLSKOPTISQSRGDRPTGPKRE	83		

Db 62 S0NHQSLSKOPSOPRBDPTGPK 86

RESULT 14

TAT_HV1A2 STANDARD: PRT: 101 AA.

AC P04614;

DT 13-AUG-1987 (Rel. 05, Created)

DT 13-AUG-1987 (Rel. 05, Last sequence update)

DT 20-AUG-2001 (Rel. 40, Last annotation update)

DE TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).

TAT

OS Human immunodeficiency virus type 1 (ARV2/SF2 isolate) (HIV-1).

OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

NCBI_Taxid=11685;

RP

SEQUENCE FROM N.A.

RA MEDLINE=65090453; Pubmed=2578227;

RA Sanchez-Pescador R., Power M.D., Barr P.J., Steimer K.S.,

RA Stempien M.M., Brown-Shimer S.L., Gee W.W., Renard A., Randolph A.,

RA Levy J.A., Dina D., Luciw P.A.;

RT "Nucleotide sequence and expression of an AIDS-associated retrovirus

(ARV-2)." ;

RL Science 227:484-492(1985).

CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE

CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND

CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR

CC

PROMOTER.

CC -1- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.

CC -----

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CC

DR EMBL: K02007; AAB59879.1; -

DR HIV: K02007; TATSF2.

DR InterPro: IPR001831; HIV_Tat.

DR Pfam: PF00539; Tat; 1.

DR PRINTS: PR00055; HIVTATDOMAIN.

KW Transcription regulation; Activator; RNA-binding; Nuclear protein;

KW

IDS SEQUENCE 101 AA; 11557 MW; 1762370A3BD641FD CRC64;

SO

Query Match 83.4%; Score 397; DB 1; Length 101;

Best Local Similarity 82.4%; Pred. No. 2.2e-34;

Matches 70; Conservative 1; Mismatches 12; Indels 2; Gaps 1;

QY 1 EVDVRLPEPMKHPGSOPTACTNCCYCKCFHCOVCFITK--AISYGRKKRRRRRRPQG 58

Db 2 EVDVRLPEPMKHPGSOPTACTNCCYCKCFHCOVCFITK--AISYGRKKRRRRRRPQG 61

QY 59 S0THQVSLSKOPSOPRBDPTGPK 83

Db 62 S0THQVSLSKOPSOPRBDPTGPK 86

RESULT 15

TAT_HV1OY STANDARD: PRT: 101 AA.

AC P20893;

DT 01-FEB-1991 (Rel. 17, Created)

DT 01-FEB-1991 (Rel. 17, Last sequence update)

DT 20-AUG-2001 (Rel. 40, Last annotation update)

DE TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).

TAT

OS Human immunodeficiency virus type 1 (OVI isolate) (HIV-1).

OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

OX NCBI_Taxid=11699;

RN

SEQUENCE FROM N.A.

RX MEDLINE=90148544; Pubmed=259749;

RA Huot T., Dazza M.C., Brun-Vezinet F., Roelants G.E., Main-Hobson S.;

RT "A highly defective HIV-1 strain isolated from a healthy Gabonese

individual presenting an atypical western blot." ;

RL AIDS 3:707-715(1989).

CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE

CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND

CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR

CC

PROMOTER.

CC -1- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.

CC -1- MISCELLANEOUS: THE OVI ISOLATE WAS TAKEN FROM THE BLOOD OF A

CC HEALTHY GABONESE INDIVIDUAL.

CC -1- MISCELLANEOUS: THE SINGLE C -> S SUBSTITUTION AT RESIDUE 22 OF THE

CC OVI TAT PROTEIN REDUCES IT INACTIVITY, BUT MAY NOT ACCOUNT FOR THE

CC AVIRULENCE OF THE VIRUS.

CC -----

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CC

DR EMBL: M26727; AAA83395.1; -

DR HIV: M26727; TATSOY1.

DR InterPro: IPR001831; HIV_Tat.

DR Pfam: PF00539; Tat; 1.

DR PRINTS: PR00055; HIVTATDOMAIN.

KW Transcription regulation; Activator; RNA-binding; Nuclear protein;

KW

IDS SEQUENCE 101 AA; 11561 MW; 83ACAC36CC4C87AD CRC64;

SO

Query Match 83.4%; Score 397; DB 1; Length 101;

Best Local Similarity 83.5%; Pred. No. 2.2e-34;

Matches 71; Conservative 2; Mismatches 10; Indels 2; Gaps 1;

QY 1 EVDVRLPEPMKHPGSOPTACTNCCYCKCFHCOVCFITK--AISYGRKKRRRRRRPQG 58

Db 2 EVDVRLPEPMKHPGSOPTACTNCCYCKCFHCOVCFITK--AISYGRKKRRRRRRPQG 61

QY 59 S0THQVSLSKOPSOPRBDPTGPK 83

Db 62 S0THQVSLSKOPSOPRBDPTGPK 86

Search completed: January 10, 2002, 15:36:01
Job time: 119 sec

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OM protein - protein search, using sw model

Run on: January 10, 2002, 15:34:02 ; Search time 21.91 Seconds

(without alignments)
554.112 Million cell updates/sec

Title: US-09-555-534-2

Perfect score: 476
Sequence: 1 EVDPRLEPWKHPGSGPRTKA.....VLSKOPTSGSRGDPGPKE 83

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPREMBL_17:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_protein:*
12: sp_virus:*
13: sp_vertibrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	437	91.8	86	12	Q74087 human immun
2	433	91.0	86	12	Q99BV4 human immun
3	432	90.8	101	12	Q92880 human immun
4	430	90.3	86	12	Q99BV5 human immun
5	429	90.1	86	12	Q57293 simian-huma
6	429	89.7	101	12	Q9DHA9 human immun
7	427	89.7	86	12	Q99BV6 human immun
8	427	89.7	86	12	Q99BV3 human immun
9	427	89.7	101	12	Q99BV7 human immun
10	426	89.5	86	12	Q99BV1 human immun
11	426	89.5	86	12	Q99BV0 human immun
12	426	89.5	101	12	Q9DHA20 human immun
13	425	89.3	101	12	Q56318 simian-huma
14	425	89.3	101	12	Q92885 human immun
15	425	89.3	101	12	Q92899 human immun
16	424	89.1	101	12	Q92893 human immun
17	424	89.1	101	12	Q99BV8 human immun
18	423	88.9	101	12	Q9DQ29 human immun
19	420	88.2	101	12	Q04191 human immun

20	420	88.2	101	12	P90265 human immun
21	420	88.2	101	12	O11405 simian-huma
22	419	88.0	101	12	O40219 human immun
23	418	87.8	101	12	O74810 human immun
24	417	87.6	101	12	O80270 human immun
25	417	87.6	101	12	O77688 human immun
26	417	87.6	101	12	O93022 human immun
27	417	87.6	101	12	O9WJV2 human immun
28	416	87.4	101	12	Q99BV9 human immun
29	415	87.2	101	12	Q95758 human immun
30	414.5	87.1	100	12	O73370 human immun
31	414	87.0	101	12	O72990 human immun
32	414	87.0	101	12	O92895 human immun
33	414	87.0	101	12	O92902 human immun
34	412	86.6	86	12	Q906V3 human immun
35	412	86.6	101	12	O04192 human immun
36	412	86.6	101	12	O74747 human immun
37	412	86.6	101	12	O93199 human immun
38	412	86.6	101	12	Q9WJV7 human immun
39	412	86.6	101	12	Q9WJV9 human immun
40	412	86.6	101	12	Q9W9E3 human immun
41	410	86.1	101	12	O72493 human immun
42	408	85.7	101	12	O71973 human immun
43	408	85.7	102	12	O91BN6 human immun
44	407	85.5	101	12	O89541 human immun
45	407	85.5	101	12	O9JAC4 human immun

ALIGNMENTS

RESULT	ID	PRELIMINARY	PRT	86 AA.
Q74087	Q74087			
AC	Q74087			
DT	01-NOV-1996 (TEMBLrel. 01, Created)			
DT	01-NOV-1996 (TEMBLrel. 01, Last sequence update)			
DT	01-JUN-2001 (TEMBLrel. 17, Last annotation update)			
DE	TAT.			
GN	TAT.			
OS	Human immunodeficiency virus type 1.			
OC	Viruses; Retrovird viruses; Retroviridae; Lentivirus.			
OX	NCBI_TaxID=11676;			
ON	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=PM213;			
RA	Cloyd M.W., Moore B.E.;			
RT	"Spectrum of Biological Properties of Human Immunodeficiency Virus (HIV-1) Isolates.";			
RL	Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=PM213;			
RA	Iwatani Y.;			
RL	Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; D86069; BAA13000.1; -			
DR	InterPro: IPR001831; HIV_Tat.			
DR	Pfam: PF00539; Tat.1			
DR	PRINTS; PR00055; HIVTRIDOMAIN.			
SQ	SEQUENCE 86 AA; 9865 MW; 4DDC56CICE269115 CRC64;			
Query Match	91.8%; Score 437; DB 12; Length 86;			
Best Local Similarity	92.9%; Pred. No. 6e-44;			
Matches	79; Conservative 0; Mismatches 4; Indels 2; Gaps 1;			
QY	1 EVDPRLEPWKHPGSGPRTKA--ISYGRKKRRQRRPPGG 58			
Db	2 EVDPRLEPWKHPGSGPRTKACNCKKCCFCGVCFTKALGISYGRKKRRQRRRAHNN 61			
QY	59 SOTHQVSLSKOPTSGSRGDPGPKE 83			
Db	62 SOTHQVSLSKOPTSGSRGDPGPKE 86			

RESULT 2
 ID 099BV4 PRELIMINARY; PRT; 86 AA.
 AC 099BV4.
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE TAT PROTEIN.
 GN TAT.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PI.2;
 RA Aldous M.C., Schwager M., Mok J.Y.Q., Yirell D.L., Leigh Brown A.J.,
 RA Fiebel K.S.;
 RT "The natural history of pediatric HIV infection suggests an
 RT association between the specificity of the cytotoxic T cells and
 RT clinical outcome."
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF324449; AAK14291.1; -
 SQ SEQUENCE 86 AA; 9842 MW; 60C7F0727C482F49 CRC64;

Query Match 91.0%; Score 433; DB 12; Length 86;
 Best Local Similarity 90.6%; Pred. No. 1.8e-43;
 Matches 77; Conservative 1; Mismatches 5; Indels 2; Gaps 1;

OY 1 EPVDRLEPMKHPGSOPTACTNCYCKKCCFHCQVCFITK--AISYGRKKRRRRPPQG 58
 DB 2 EPVDRLEPMKHPGSOPTACTNCYCKKCCFHCQVCFITKGLISYGRKKRRRRPPQS 61
 OY 59 SOTHQVSLSKOPTSQRDPGPKKE 83
 DB 62 SOTHQVSLSKOPTSQRDPGPKKE 86

RESULT 3
 ID 092880 PRELIMINARY; PRT; 101 AA.
 AC 092880;
 DT 01-NOV-1998 (TREMBlrel. 08, Created)
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE TAT PROTEIN.
 GN TAT.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MC200;
 RA Oelrichs R.B., Mophee D.A., Deacon N.J.;
 RT "Biological cloning and full-length sequence of two Australian HIV-1
 RT primary clinical isolates with distinct cellular tropism and
 RT cytopathicity."
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF042100; AAD03194.1; -
 DR InterPro; IPR001831; HIV_Tat.
 DR Pfam; PF00539; Tat; 1.
 DR PRINTS; PR00055; HIVTATDOMAIN.
 SQ SEQUENCE 101 AA; 11593 MW; A9F467BD68399235 CRC64;

Query Match 90.8%; Score 432; DB 12; Length 101;
 Best Local Similarity 90.6%; Pred. No. 2.6e-43;
 Matches 77; Conservative 1; Mismatches 5; Indels 2; Gaps 1;
 OY 1 EPVDRLEPMKHPGSOPTACTNCYCKKCCFHCQVCFITK--AISYGRKKRRRRPPQG 58
 DB 2 EPVDRLEPMKHPGSOPTACTNCYCKKCCFHCQVCFITKGLISYGRKKRRRRPPQS 61

DB 2 EPVDRLEPMKHPGSOPTACTNCYCKKCCFHCQVCFITKGLISYGRKKRRRRPPAD 61
 OY 59 SOTHQVSLSKOPTSQRDPGPKKE 83
 DB 62 SOTHQVSLSKOPTSQRDPGPKKE 86

RESULT 4
 ID 099BV5 PRELIMINARY; PRT; 86 AA.
 AC 099BV5.
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE TAT PROTEIN.
 GN TAT.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PI.2.1;
 RA Aldous M.C., Schwager M., Mok J.Y.Q., Yirell D.L., Leigh Brown A.J.,
 RA Fiebel K.S.;
 RT "The natural history of pediatric HIV infection suggests an
 RT association between the specificity of the cytotoxic T cells and
 RT clinical outcome."
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF324448; AAK14290.1; -
 SQ SEQUENCE 86 AA; 9828 MW; C1C6E1727D928438 CRC64;

Query Match 90.3%; Score 430; DB 12; Length 86;
 Best Local Similarity 89.4%; Pred. No. 4e-43;
 Matches 76; Conservative 2; Mismatches 5; Indels 2; Gaps 1;

OY 1 EPVDRLEPMKHPGSOPTACTNCYCKKCCFHCQVCFITK--AISYGRKKRRRRPPQG 58
 DB 2 EPVDRLEPMKHPGSOPTACTNCYCKKCCFHCQVCFITKGLISYGRKKRRRRPPQS 61
 OY 59 SOTHQVSLSKOPTSQRDPGPKKE 83
 DB 62 SOTHQVSLSKOPTSQRDPGPKKE 86

RESULT 5
 ID 057293 PRELIMINARY; PRT; 86 AA.
 AC 057293;
 DT 01-JUN-1998 (TREMBlrel. 06, Created)
 DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE TAT PROTEIN.
 GN TAT.
 OS Simian-Human immunodeficiency virus.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=57667;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SHIV-4, HXBC2;
 RA Cayabyab M., Karlsson G.B., Etmed-Moghadam B., Hofmann W.,
 RA Halloran M., Axelholm M.W., Letvin N.L., Sodroski J.G.;
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SHIV-4, HXBC2;
 RX MEDLINE=92309177; PubMed=1613662;
 RA Li J., Lord C.I., Haseltine W., Letvin N.L., Sodroski J.;
 RT "Infection of cynomolgus monkeys with a chimeric HIV-1/SIVmac virus
 RT that expresses the HIV-1 envelope glycoproteins."
 RL J. Acquir. Immune Defic. Syndr. 5:639-646(1992).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SHIV-4, HXBC2;

DT	01-JUN-2001 (Tremblrel, 17, Created)
DT	01-JUN-2001 (Tremblrel, 17, Last sequence update)

DT 01-JUN-2001 (TREMblrel. 17, last annotation update)
DE TAT PROTEIN.
GN TAT.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=P.2;
RA Aldous M.C., Schwager M., Mok J.Y.Q., Virrell D.L., Leigh Brown A.J.,
RA Froebel K.S.;
RT "The natural history of pediatric HIV infection suggests an
RT association between the specificity of the cytotoxic T cells and
RT clinical outcome."
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF324446; AAK14285.1; -
SQ SEQUENCE 101 AA; 11517 MW; 03AB48CC28C9DE2 CRC64;

Query Match 89.7%; Score 427; DB 12; Length 101;
Best Local Similarity 90.6%; Pred. No. 1e-42;
Matches 77; Conservative 0; Mismatches 6; Indels 2; Gaps 1;

OY 1 EPVDPLRLEPMKHPGSPKACTNCYCKKCCFHQVCFTK--AISYGRKKRRRRPPQG 58
|||||
DB 2 EPVDPLRLEPMKHPGSPKACTNCYCKKCCFHQVCFTKGLGISYGRKKRRRRAPD 61
OY 59 SOTHQVSLSKOPTSOSRGDPTGPK 83
|||||
DB 62 SOTHQVSLSKOPTSOSRGDPTGPK 86

RESULT 10
O99BWL PRELIMINARY; PRT; 86 AA.
AC O99BWL;
DT 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 17, last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, last annotation update)
DE TAT PROTEIN.
GN TAT.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=P.2;
RA Aldous M.C., Schwager M., Mok J.Y.Q., Virrell D.L., Leigh Brown A.J.,
RA Froebel K.S.;
RT "The natural history of pediatric HIV infection suggests an
RT association between the specificity of the cytotoxic T cells and
RT clinical outcome."
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF324440; AAK14283.1; -
SQ SEQUENCE 86 AA; 9725 MW; 3A1C9D514983A7A8 CRC64;

Query Match 89.5%; Score 426; DB 12; Length 86;
Best Local Similarity 89.4%; Pred. No. 1.2e-42;
Matches 76; Conservative 1; Mismatches 6; Indels 2; Gaps 1;

OY 1 EPVDPLRLEPMKHPGSPKACTNCYCKKCCFHQVCFTK--AISYGRKKRRRRPPQG 58
|||||
DB 2 EPVDPLRLEPMKHPGSPKACTNCYCKKCCFHQVCFTKGLGISYGRKKRRRRAPD 61
OY 59 SOTHQVSLSKOPTSOSRGDPTGPK 83
|||||
DB 62 SOTHQVSLSKOPTSOSRGDPTGPK 86

RESULT 11
O99BWO PRELIMINARY; PRT; 86 AA.

AC O99BWO;
DT 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 17, last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, last annotation update)
DE TAT PROTEIN.
GN TAT.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=P.1;
RA Aldous M.C., Schwager M., Mok J.Y.Q., Virrell D.L., Leigh Brown A.J.,
RA Froebel K.S.;
RT "The natural history of pediatric HIV infection suggests an
RT association between the specificity of the cytotoxic T cells and
RT clinical outcome."
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF324442; AAK14285.1; -
SQ SEQUENCE 86 AA; 9803 MW; 9B0D8E524AEC1B0E CRC64;

Query Match 89.5%; Score 426; DB 12; Length 86;
Best Local Similarity 90.6%; Pred. No. 1.2e-42;
Matches 77; Conservative 0; Mismatches 6; Indels 2; Gaps 1;

OY 1 EPVDPLRLEPMKHPGSPKACTNCYCKKCCFHQVCFTK--ISYGRKKRRRRPPQG 58
|||||
DB 2 EPVDPLRLEPMKHPGSPKACTNCYCKKCCFHQVCFTKGLGISYGRKKRRRRTPD 61
OY 59 SOTHQVSLSKOPTSOSRGDPTGPK 83
|||||
DB 62 SOTHQVSLSKOPTSOSRGDPTGPK 86

RESULT 12
O9DH20 PRELIMINARY; PRT; 101 AA.
AC O9DH20;
DT 01-MAR-2001 (TREMblrel. 16, Created)
DT 01-MAR-2001 (TREMblrel. 16, last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, last annotation update)
DE TAT PROTEIN.
GN TAT.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20457217; PubMed=11000225;
RA Yuste E., Lopez-Galindez C., Domingo E.;
RT "Unusual distribution of mutations associated with serial Bottleneck
RT passages of Human Immunodeficiency Virus Type 1."
RL J. Virol. 74:9546-9552(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Yuste E., Lopez-Galindez C., Domingo E.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF256211; AAG16848.1; -
DR EMBL: AF256204; AAG16788.1; -
DR EMBL: AF256205; AAG16797.1; -
DR EMBL: AF256206; AAG16805.1; -
DR EMBL: AF256207; AAG16814.1; -
DR EMBL: AF256208; AAG16822.1; -
DR InterPro: IPR001831; HIV_Tat.
DR Pfam: PF00539; Tat. 1.
DR PRINTS: PR00055; HIVTATDOMAIN.
SQ SEQUENCE 101 AA; 11453 MW; 831E576C7E82C649 CRC64;

Query Match 89.5%; Score 426; DB 12; Length 101;
Best Local Similarity 89.4%; Pred. No. 1.3e-42;
Matches 76; Conservative 1; Mismatches 6; Indels 2; Gaps 1;

QY 1 EPVDPRLPEPMKHPGSOPTACTNCTCKKCCFHCQVCFTTK--AISYGRKKRRORRRPPQG 58
 DB 2 EPVDPRLPEPMKHPGSOPTACTNCTCKKCCFHCQVCFTTKGLISYGRKKRRORRRAPQD 61
 QY 59 SOTHOVSLSKOPTSQSRGDDPTGPKE 83
 DB 62 SOTHOVSLSKOPTSQSRGDDPTGPKE 86

RESULT 13

ID 056318 PRELIMINARY; PRT; 101 AA.

AC 056318;
 DT 01-JUN-1998 (TREMBlrel. 06, Created)
 DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE STRAIN SHIV-89.6, COMPLETE GENOME.

OS "TAT".
 OC Simian-Human immunodeficiency virus.
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.

OX NCBI_TaxID=57667;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN-SHIV-89.6;
 RX MEDLINE=96186751; PubMed=8627800;

RA Reimann K.A., Li J.T., Voss G., Lekutis C., Tenner-Racz K., Racz P.,
 RA Lin W., Montefiori D.C., Lee-Parritz D.E., Lu Y., Collman R.G.,
 RA Sodroski J., Letvin N.L.;

RT "An env gene derived from a primary human immunodeficiency virus type
 RT 1 isolate confers high in vivo replicative capacity to a chimeric

RT simian/human immunodeficiency virus in rhesus monkeys.";
 DT J. Virol. 70:3198-3206(1996).

RN [2]
 RP SEQUENCE FROM N.A.

RC STRAIN-SHIV-89.6;
 RA Reimann K.A., Li J.T., Voss G., Lekutis C., Tenner-Racz K., Racz P.,

RA Lin W., Montefiori D.C., Lee-Parritz D.E., Lu Y., Collman R.G.,
 RA Sodroski J., Letvin N.L.;

RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF038398; AAB9963.1; -

DR InterPro: IPR001831; HIV_Tat.
 DR Pfam: PF00539; Tat; 1.

DR PRINTS: PR00055; HIVTATDOMAIN.
 DR SEQUENCE 101 AA; 11629 MW; ACC85C20970DDP9 CRC64;

SQ

Query Match 89.3%; Score 425; DB 12; Length 101;
 Best Local Similarity 89.4%; Pred. No. 1.7e-42;

Matches 76; Conservative 2; Mismatches 5; Indels 2; Gaps 1;

QY 1 EPVDPRLPEPMKHPGSOPTACTNCTCKKCCFHCQVCFTTKA--ISYGRKKRRORRRPPQG 58
 DB 2 EPVDPRLPEPMKHPGSOPTACTNCTCKKCCFHCQVCFTTKGLISYGRKKRRORRRAPQD 61

QY 59 SOTHOVSLSKOPTSQSRGDDPTGPKE 83
 DB 62 SOTHOVSLSKOPTSQSRGDDPTGPKE 86

RESULT 14

ID 092885 PRELIMINARY; PRT; 101 AA.

AC 092885;
 DT 01-NOV-1998 (TREMBlrel. 08, Created)

DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)

DE TAT PROTEIN.
 GN TAT.

OS Human immunodeficiency virus type 1.
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.

OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN-MBC925;
 RA Oelrichs R.B., McPhee D.A., Deacon N.J.;

RT "Biological cloning and full-length sequence of two Australian HIV-1
 RT primary clinical isolates with distinct cellular tropism and

RT cytopathicity";
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF042101; AAD03203.1; -
 DR InterPro: IPR001831; HIV_Tat.

DR Pfam: PF00539; Tat; 1.
 DR PRINTS: PR00055; HIVTATDOMAIN.

DR SEQUENCE 101 AA; 11576 MW; 93352253792B3FB2 CRC64;

RESULT 15

ID 092899 PRELIMINARY; PRT; 101 AA.

AC 092899;
 DT 01-NOV-1998 (TREMBlrel. 08, Created)

DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)

DE TAT PROTEIN.
 GN TAT.

OS Human immunodeficiency virus type 1.
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.

OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN-MBCD36;
 RA Oelrichs R.B., McPhee D.A., Deacon N.J.;

RT "Genomic sequence of HIV-1 from four members of the Sydney Blood Bank
 RT Cohort of long term non-progressors.";

RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF042105; AAD03236.1; -

DR InterPro: IPR001831; HIV_Tat.
 DR Pfam: PF00539; Tat; 1.

DR PRINTS: PR00055; HIVTATDOMAIN.
 DR SEQUENCE 101 AA; 11512 MW; 440B807D4FA8738E CRC64;

SQ

Query Match 89.3%; Score 425; DB 12; Length 101;
 Best Local Similarity 87.1%; Pred. No. 1.7e-42;

Matches 74; Conservative 5; Mismatches 4; Indels 2; Gaps 1;

QY 1 EPVDPRLPEPMKHPGSOPTACTNCTCKKCCFHCQVCFTTK--AISYGRKKRRORRRPPQG 58
 DB 2 EPVDPRLPEPMKHPGSOPTACTNCTCKKCCFHCQVCFTTKGLISYGRKKRRORRRAPQD 61

QY 59 SOTHOVSLSKOPTSQSRGDDPTGPKE 83
 DB 62 SOTHOVSLSKOPTSQSRGDDPTGPKE 86

Search completed: January 10, 2002, 15:35:44
 Job time: 102 sec

Thu Jan 10 15:38:07 2002

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